

1. FULL LENGTH PLASMID: 1-9395 (GENBANK ACCESSION NUMBER AF 121950)

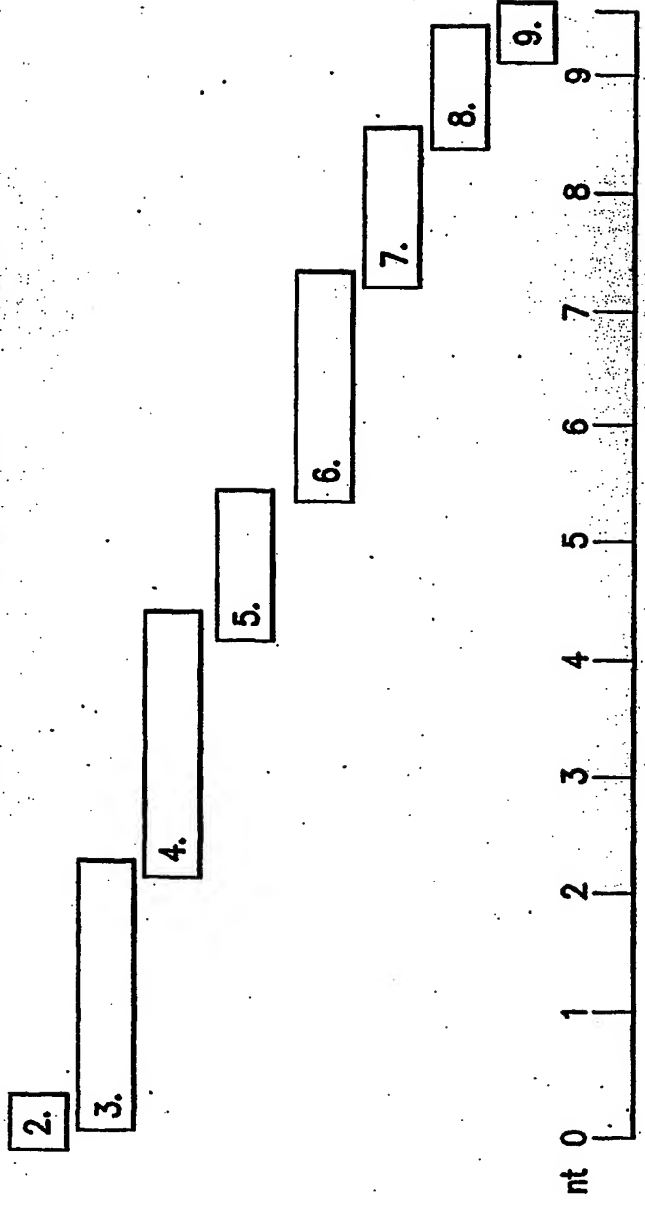


FIG. 1A



FIG.1B

0.05

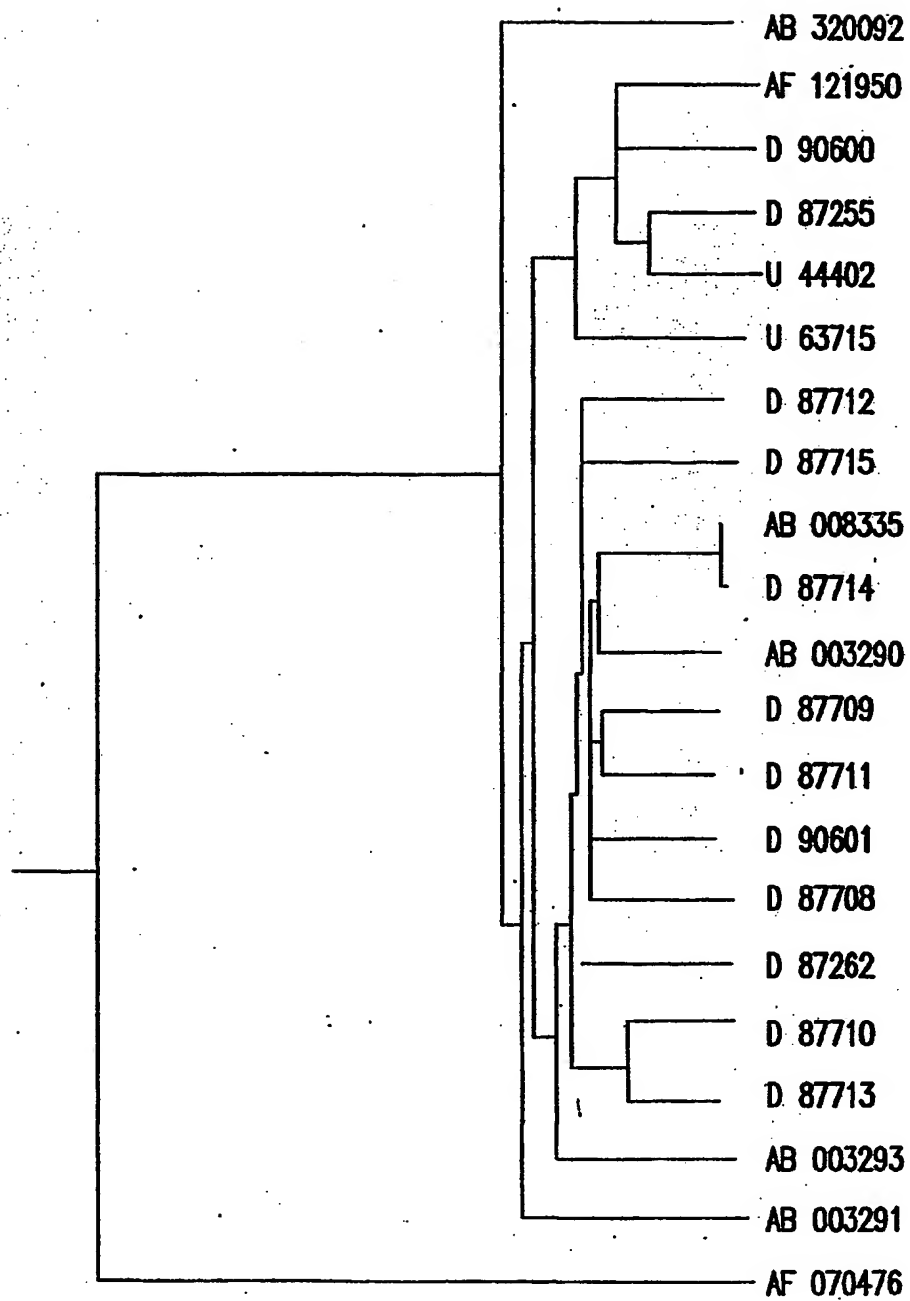


FIG.2

0.05

GBV-B

GBV-C

HCV

FIG. 3A

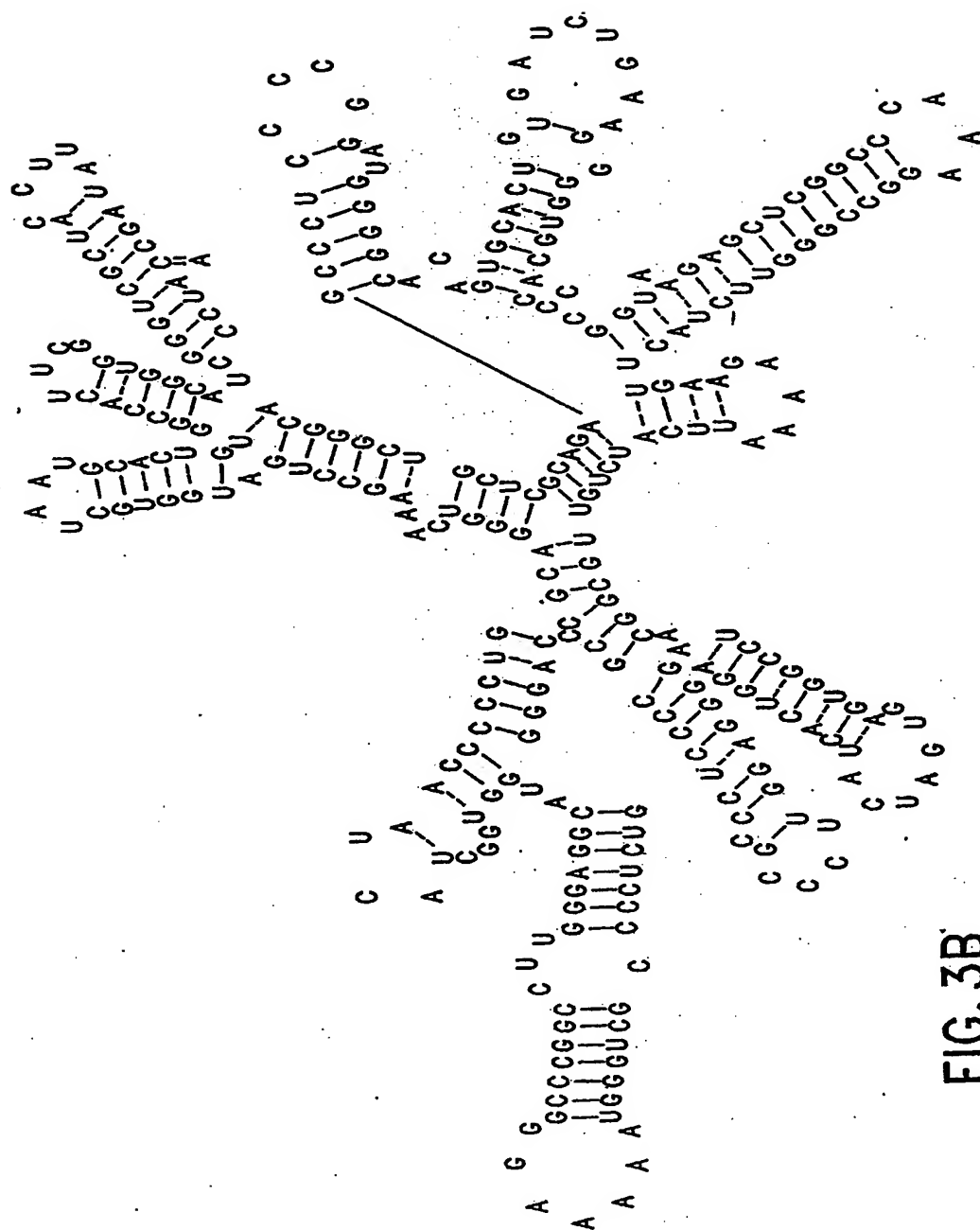


FIG. 3B

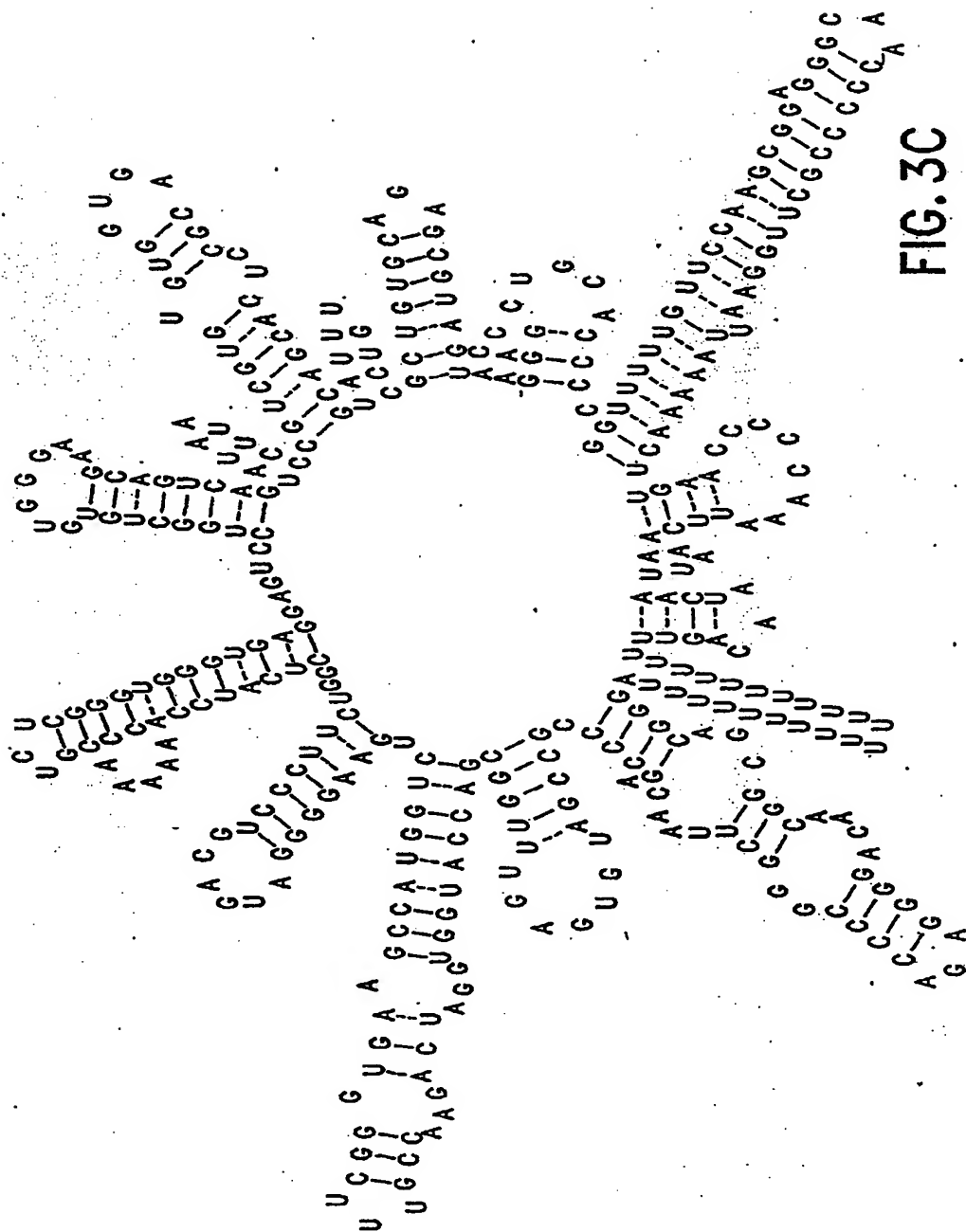


FIG. 3C

RELATIVE GBV-C RNA CONCENTRATION IN CELL CULTURE SUPERNATANT FLUID.

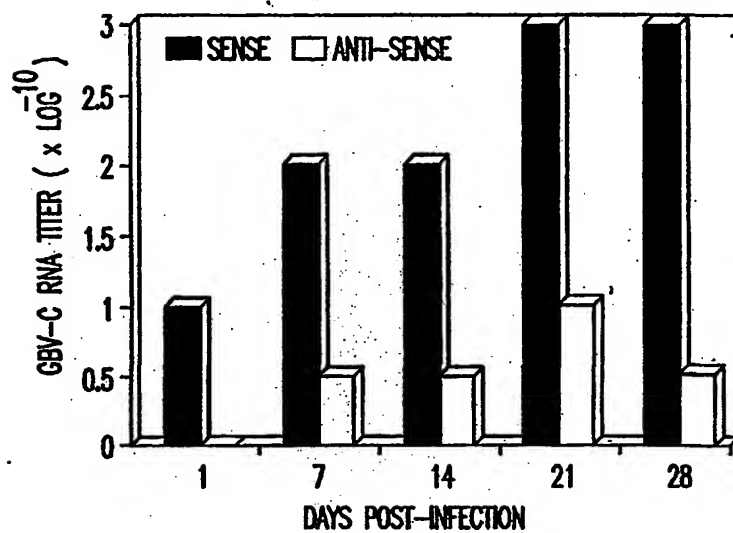


FIG. 4A

RELATIVE GBV-C RNA CONCENTRATION IN CELL LYSATE.

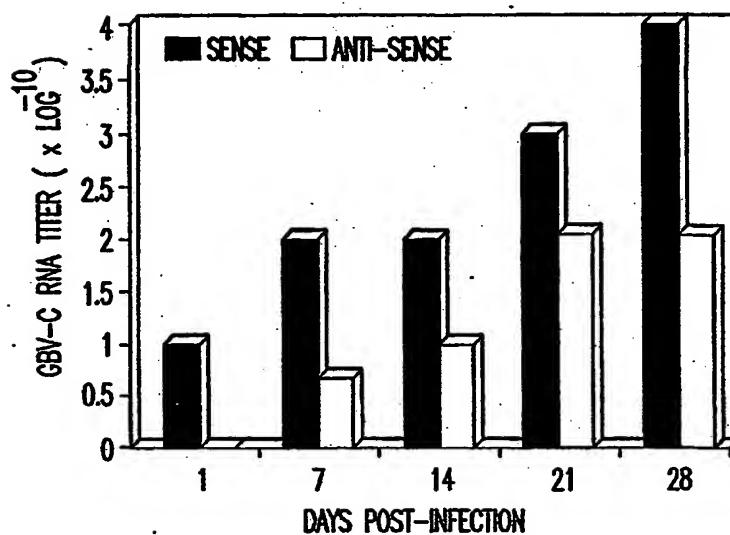


FIG. 4B

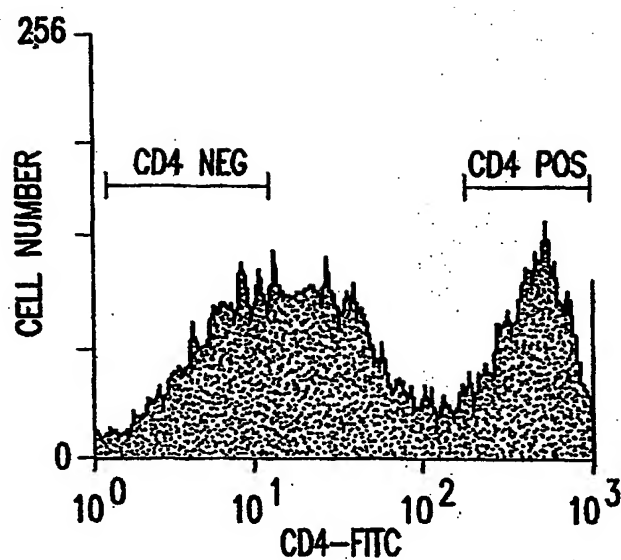
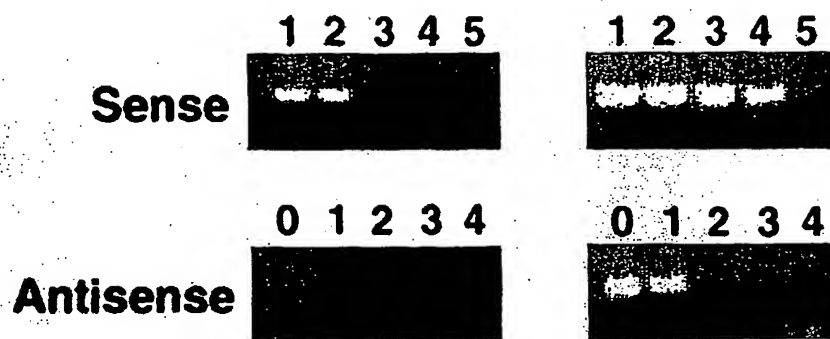


FIG.5

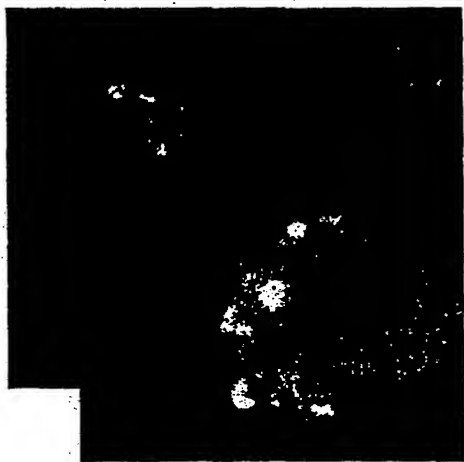


FIG. 6A



FIG. 6B



FIG. 6C

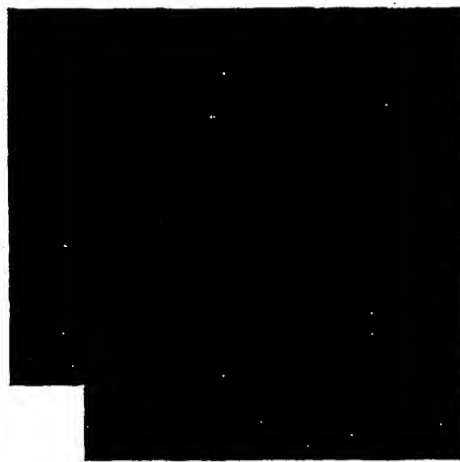


FIG. 6D

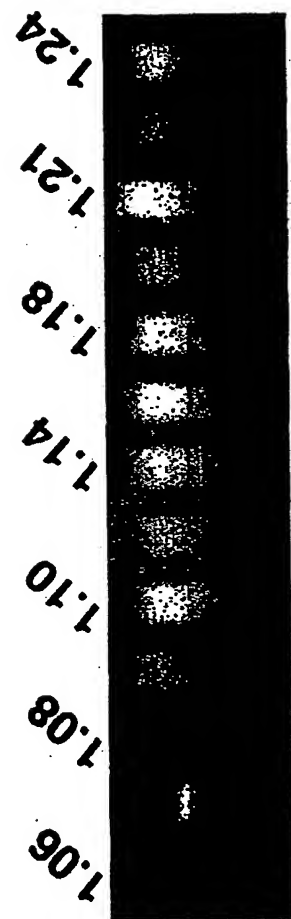


FIG. 7A

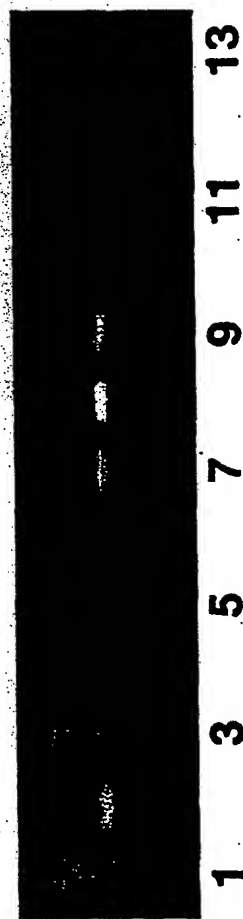


FIG. 7B



FIG.8A



FIG.8B

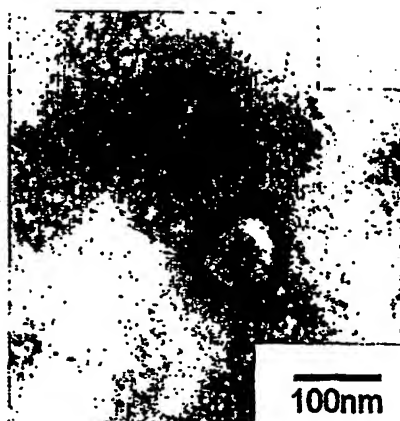


FIG.8C

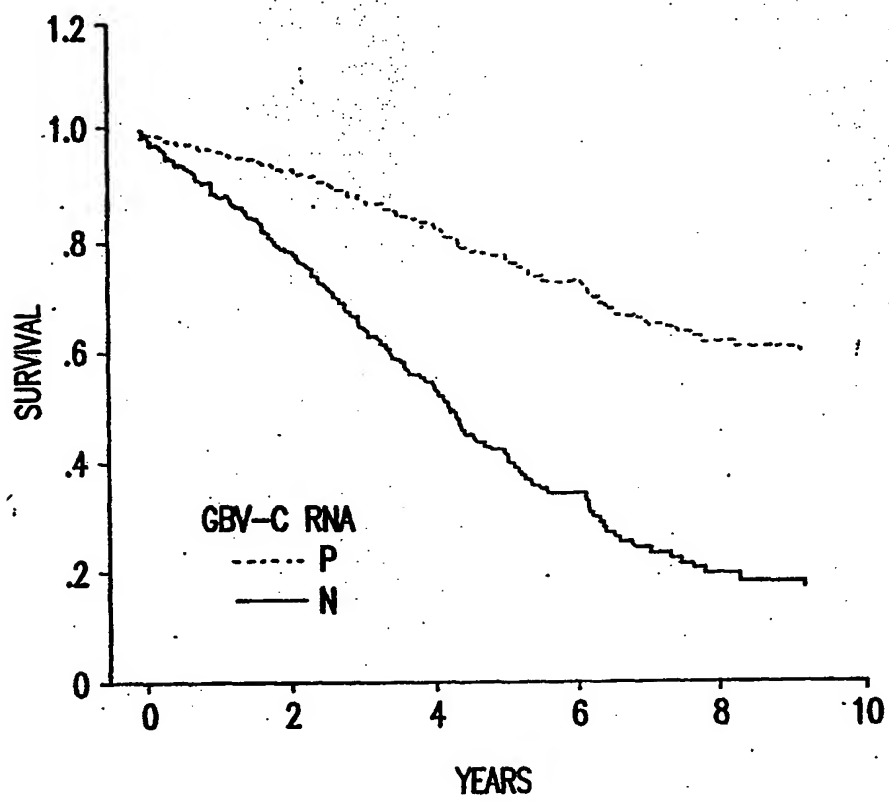


FIG.9

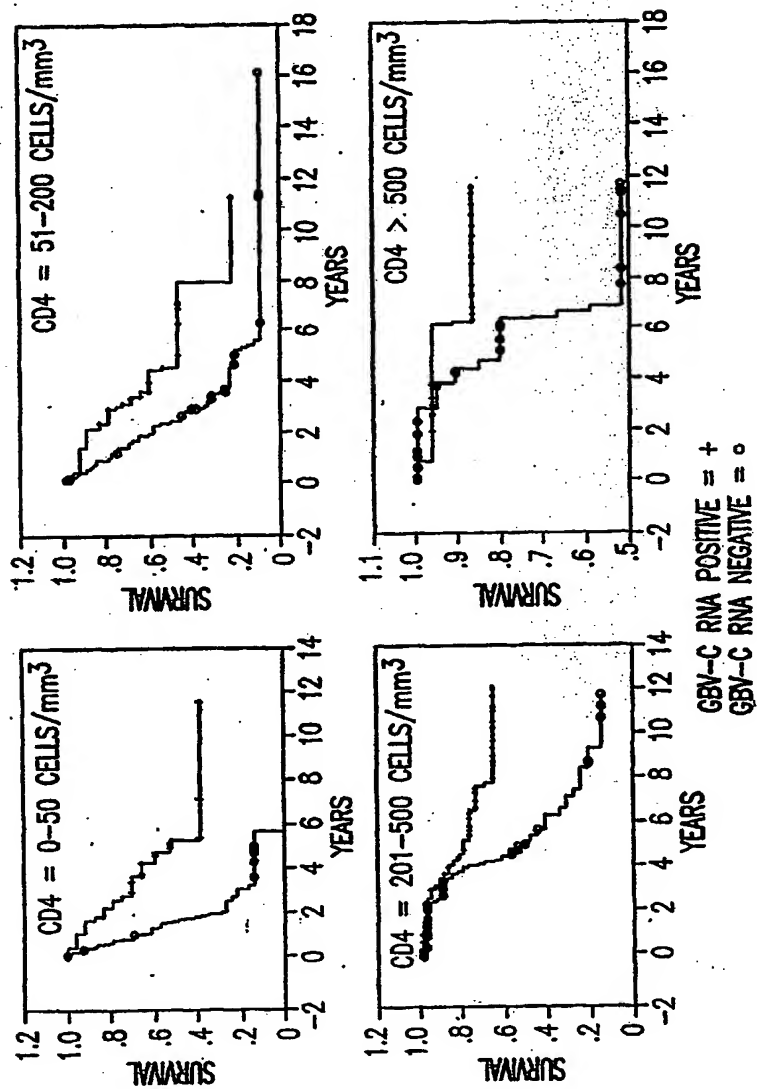


FIG.10

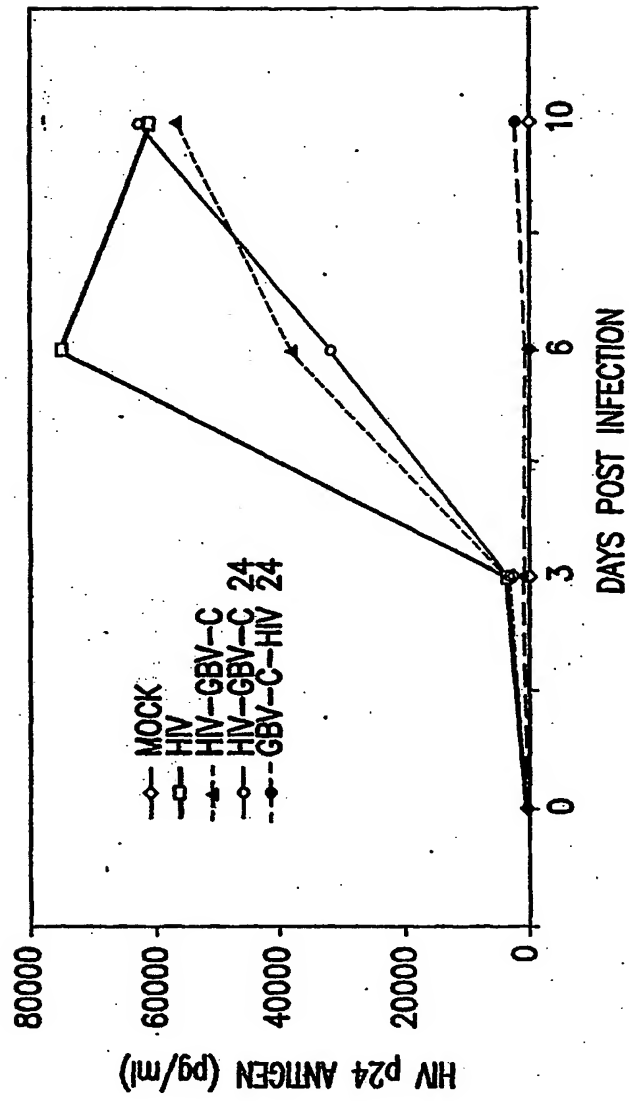


FIG. 11

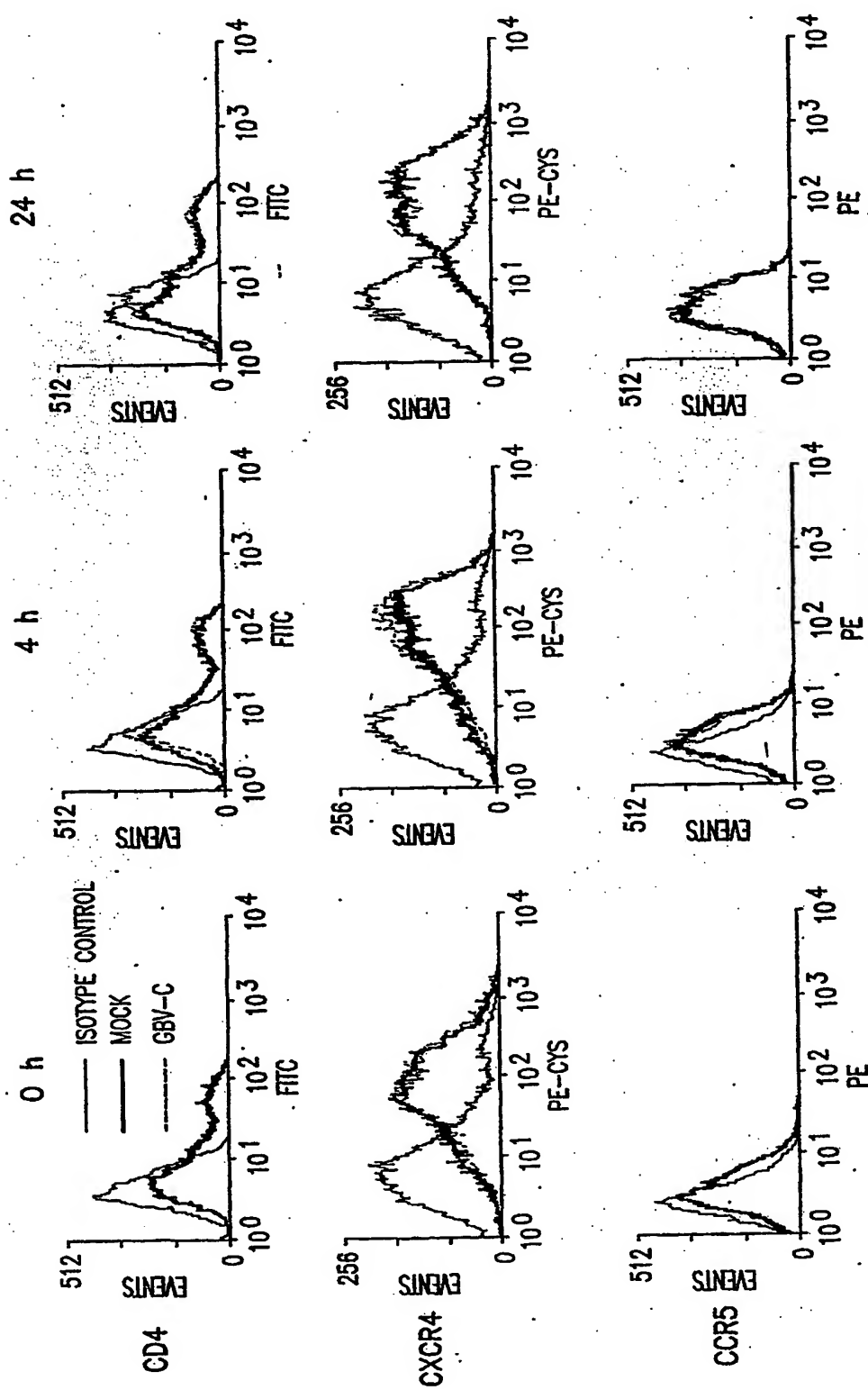


FIG.12

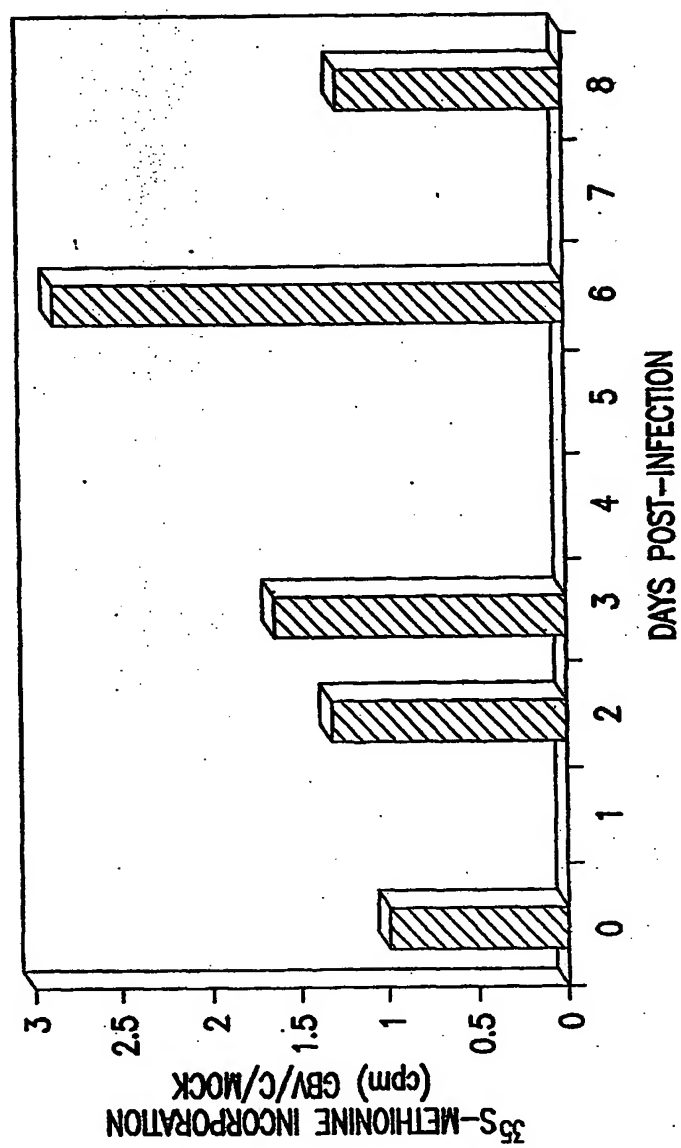


FIG. 13

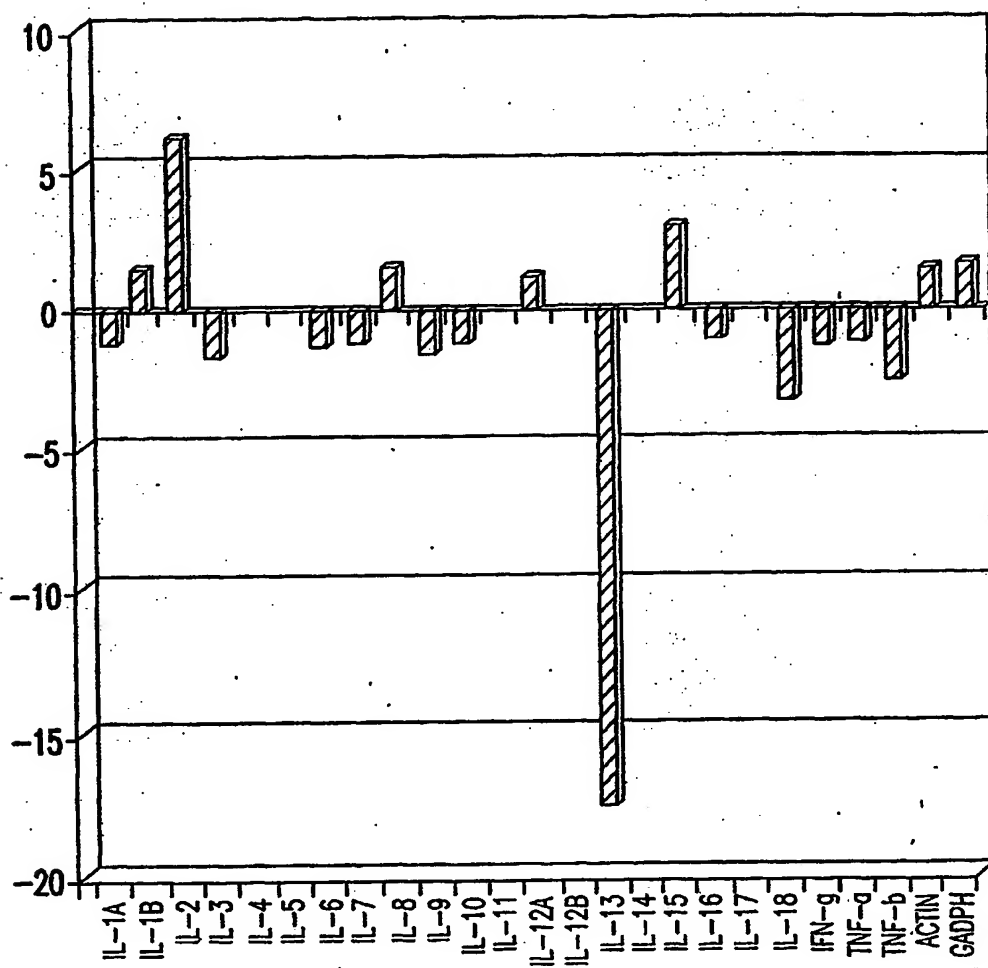


FIG. 14

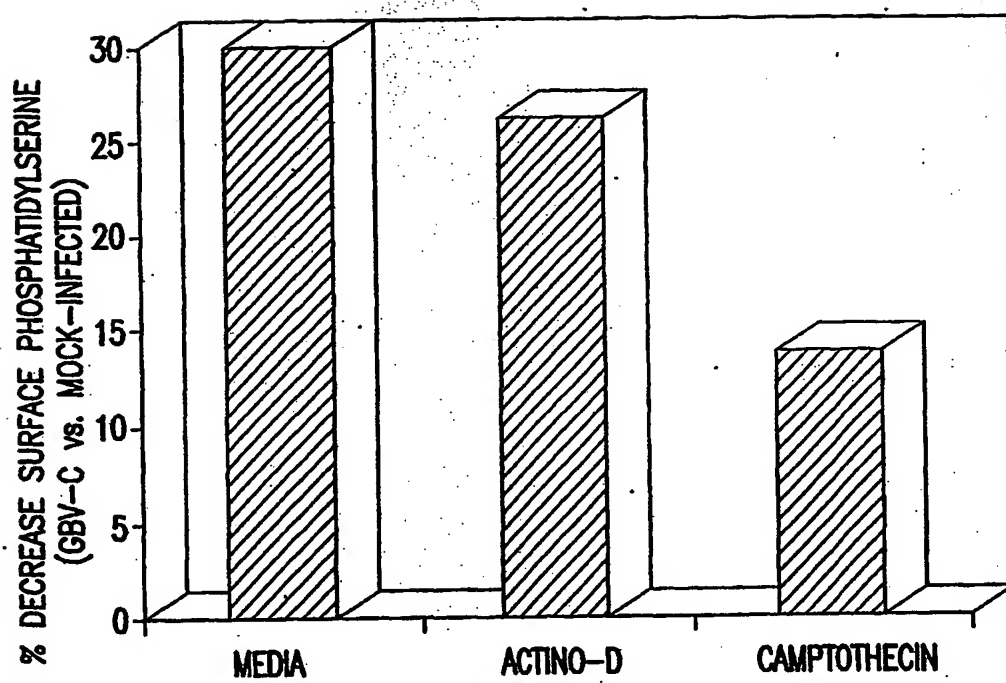


FIG. 15

Figure 4.¹⁶

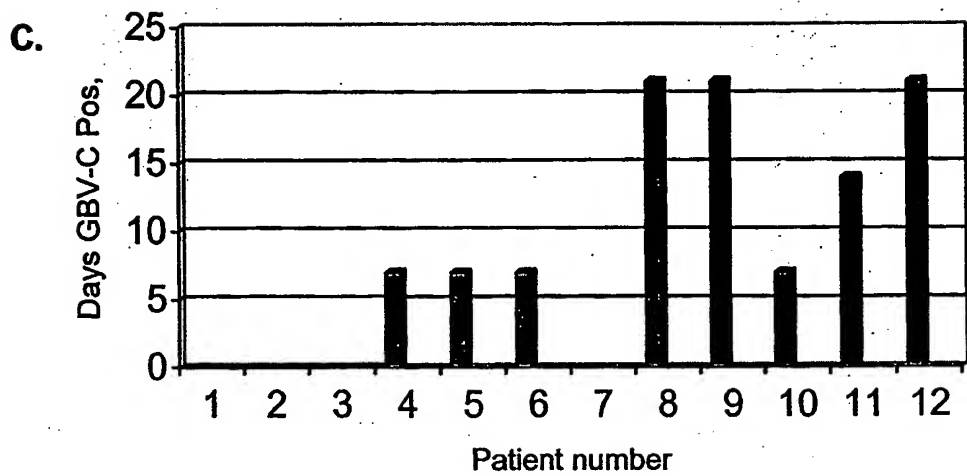
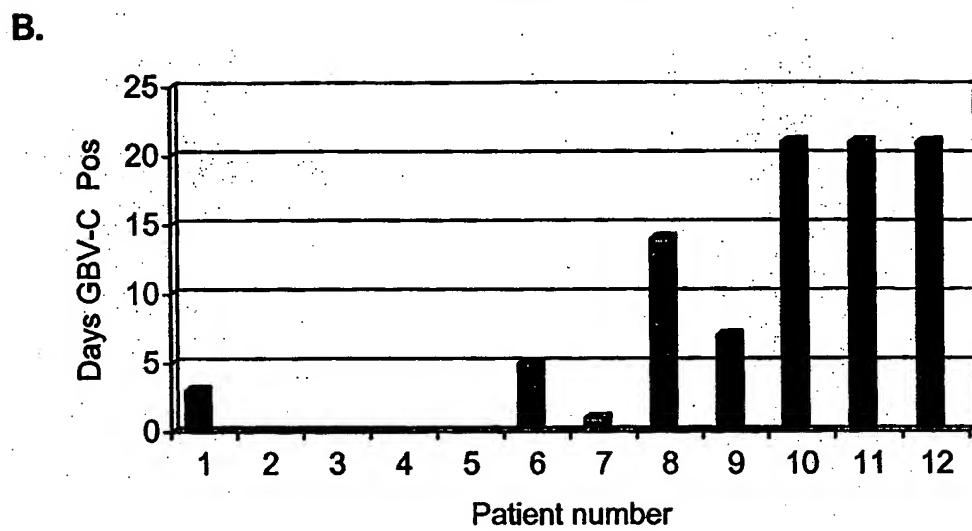
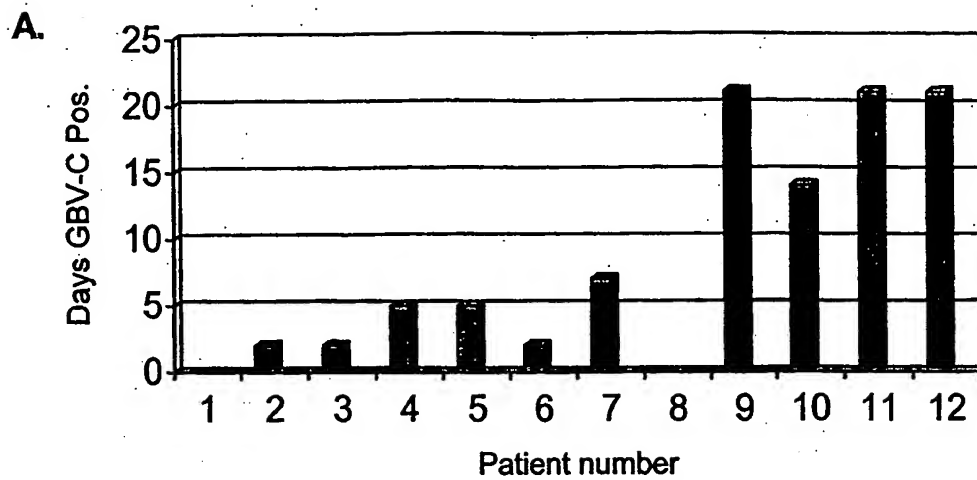
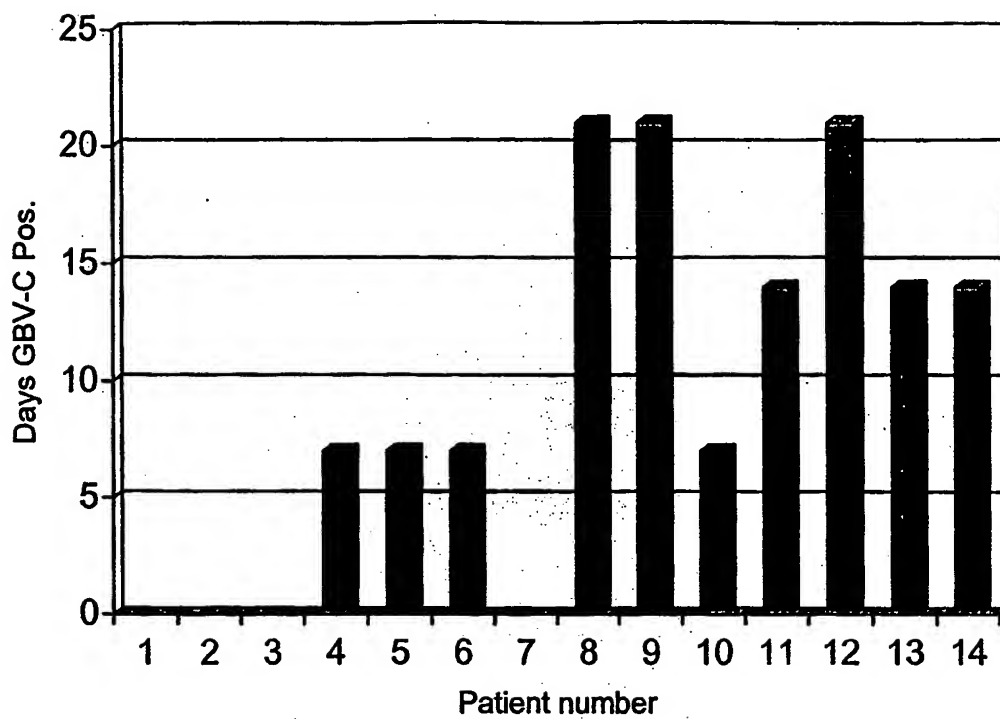


Figure 2. ¹⁷



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Figure 3.

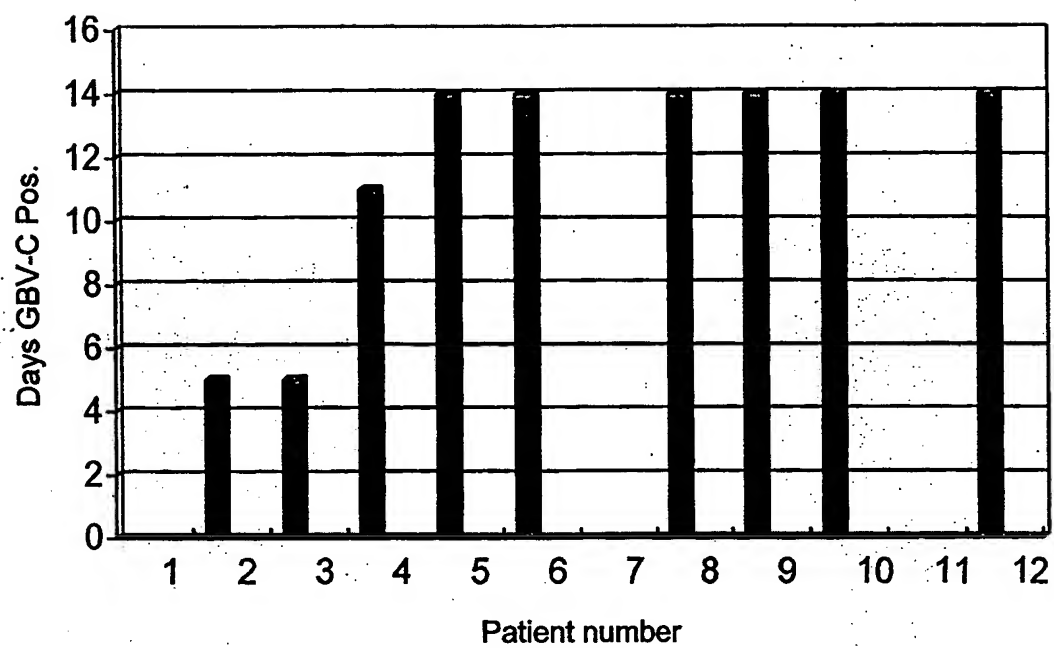
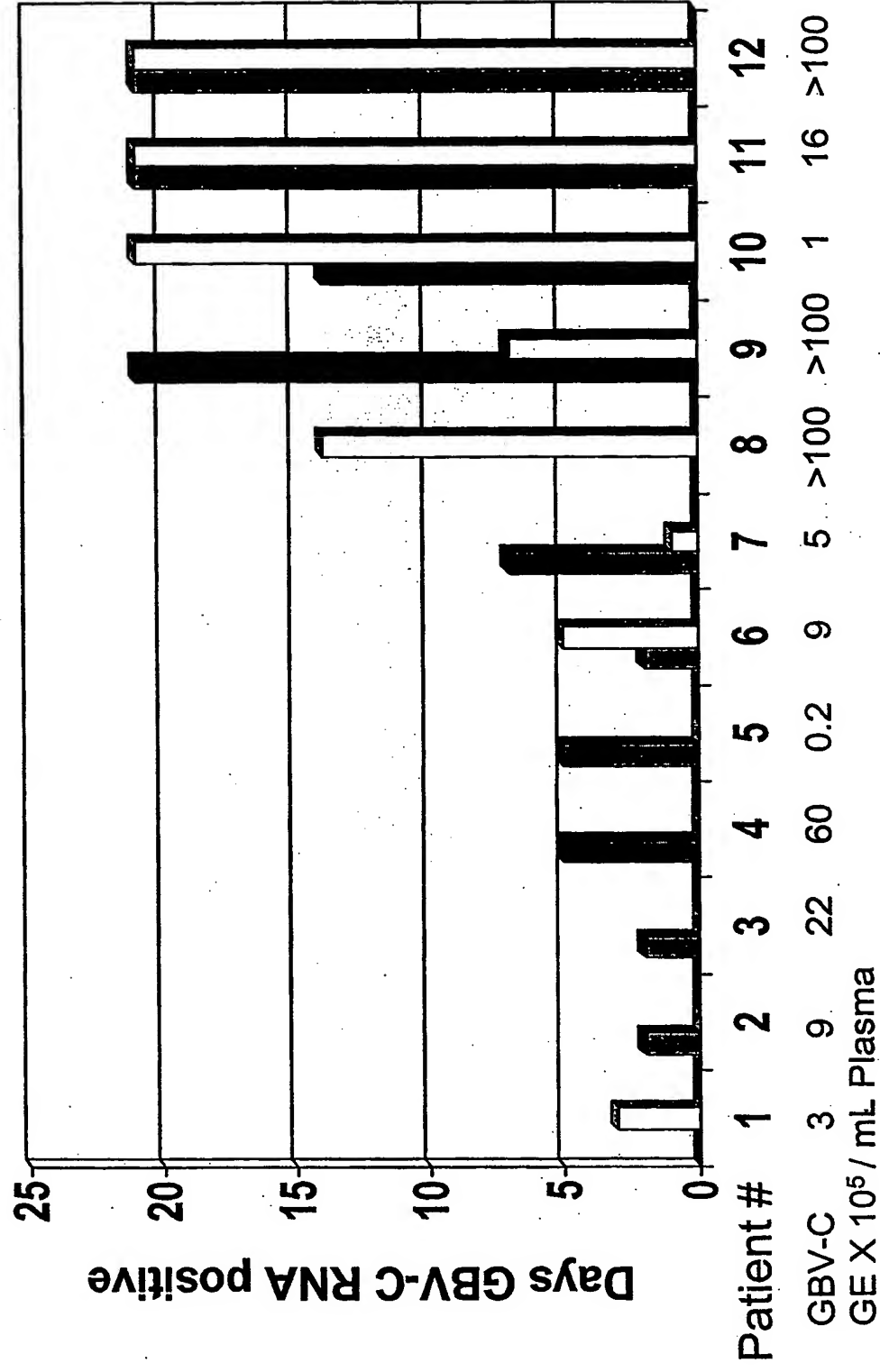


Figure 1A: GBV-C replication in PBMC cultures

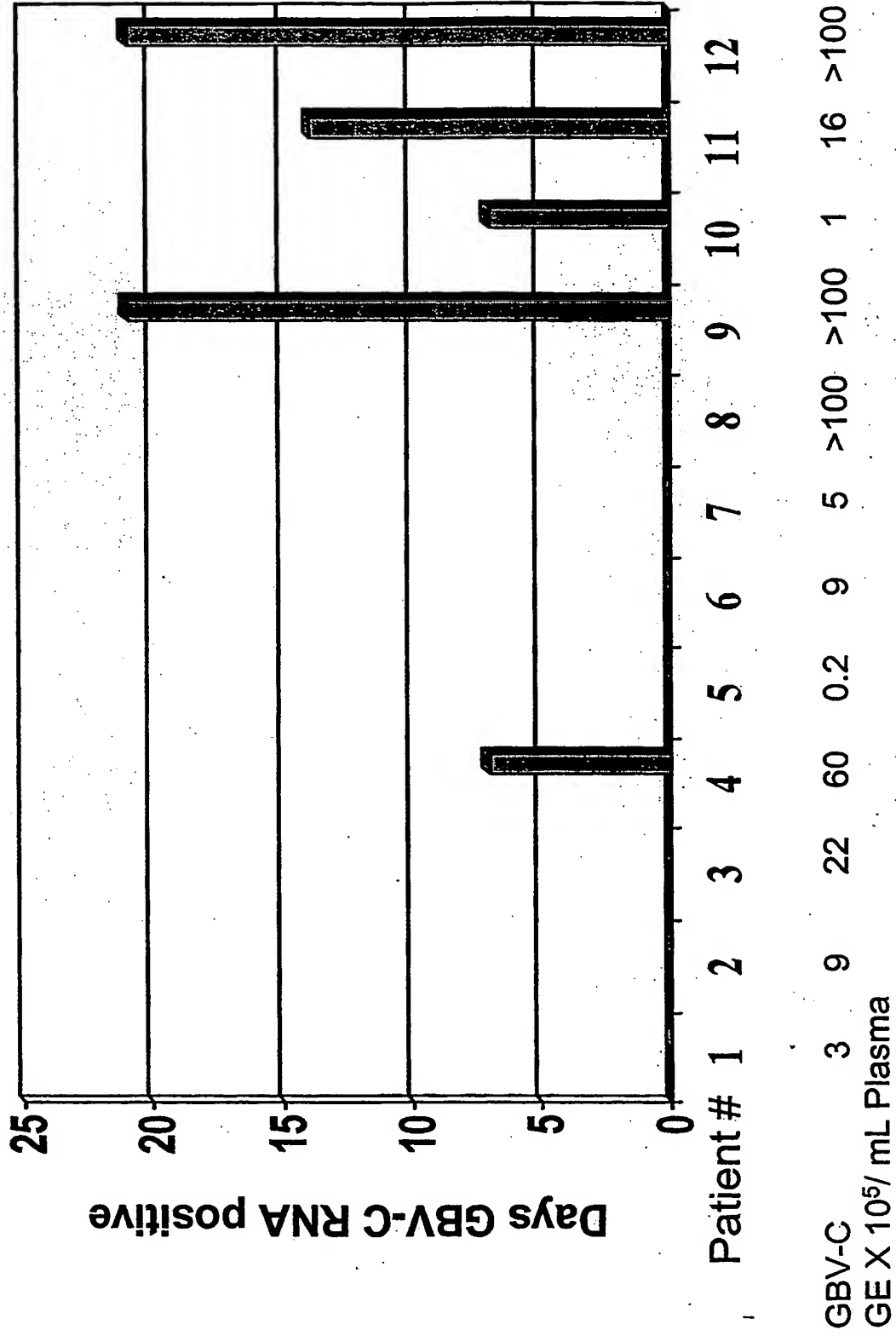


Open bars = patient PBMCs cultured with healthy donor PBMCs

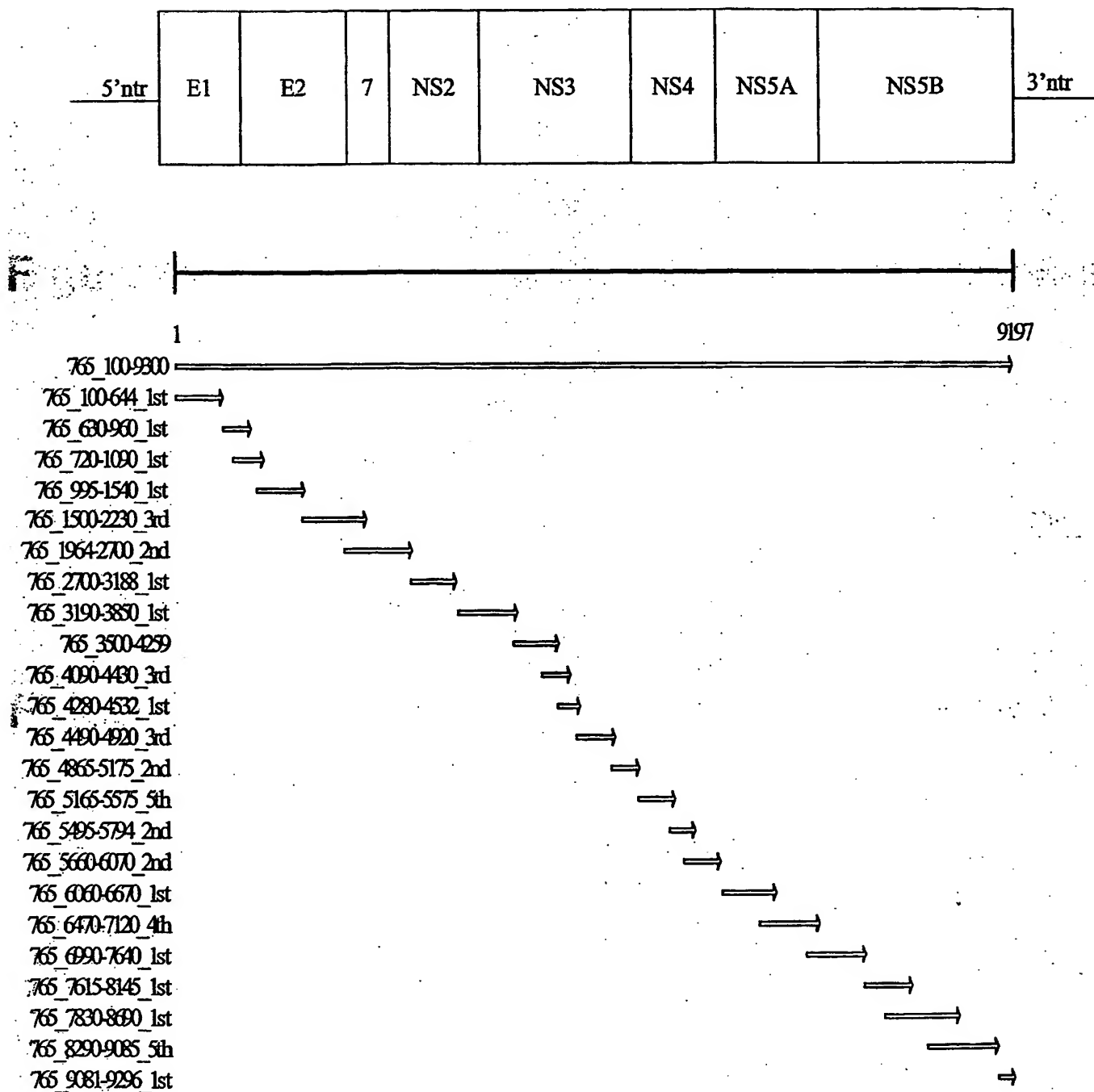
Solid bars = patient PBMCs cultured without donor PBMCs

19

Figure 1B: Plasma GBV-C infection in donor PBMCs



²⁰
Figure 2: Sequence of full-length GBV-C genome
(patient #12 – isolate 765)



21
Figure 3: Phylogenetic Tree of GBV-C Nucleotide Sequences

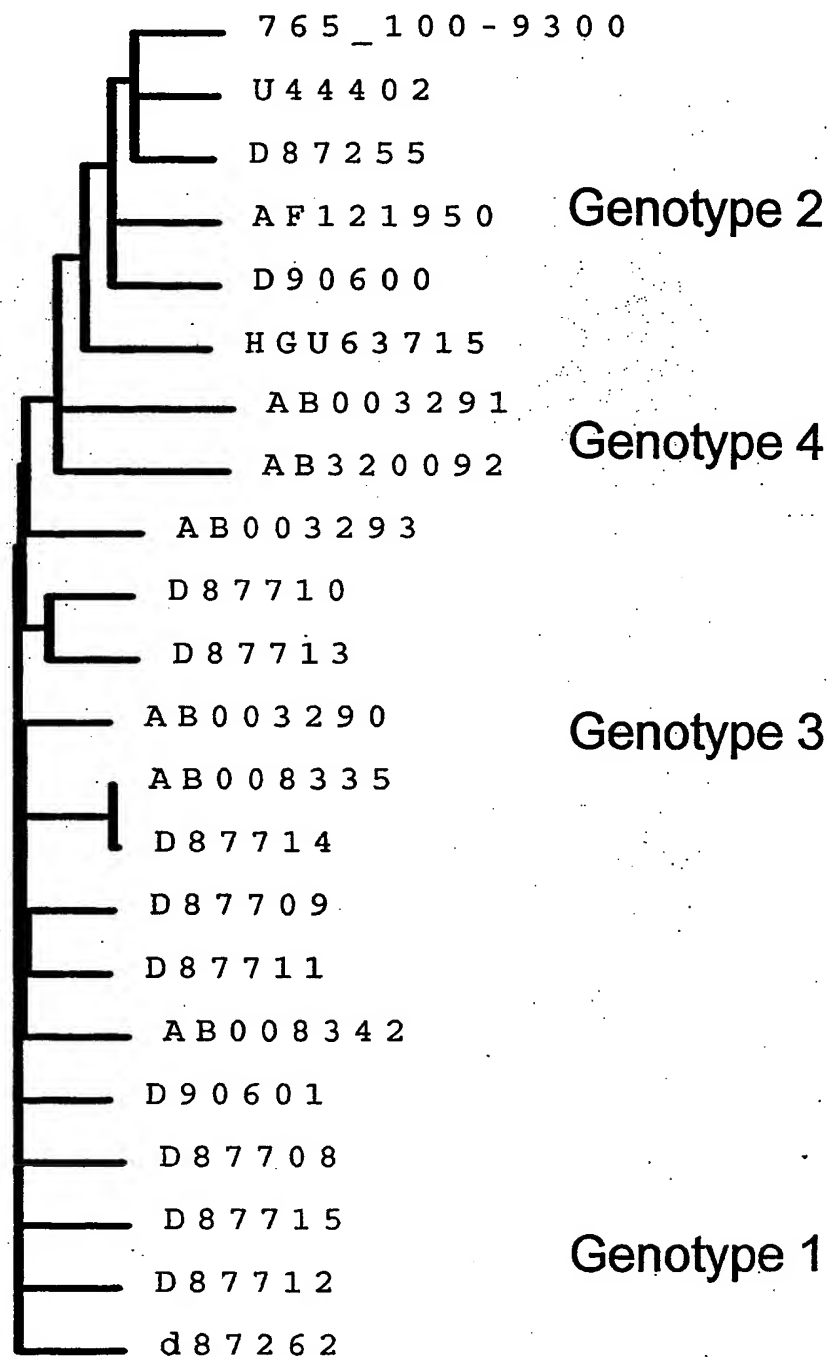
0 . 0 5



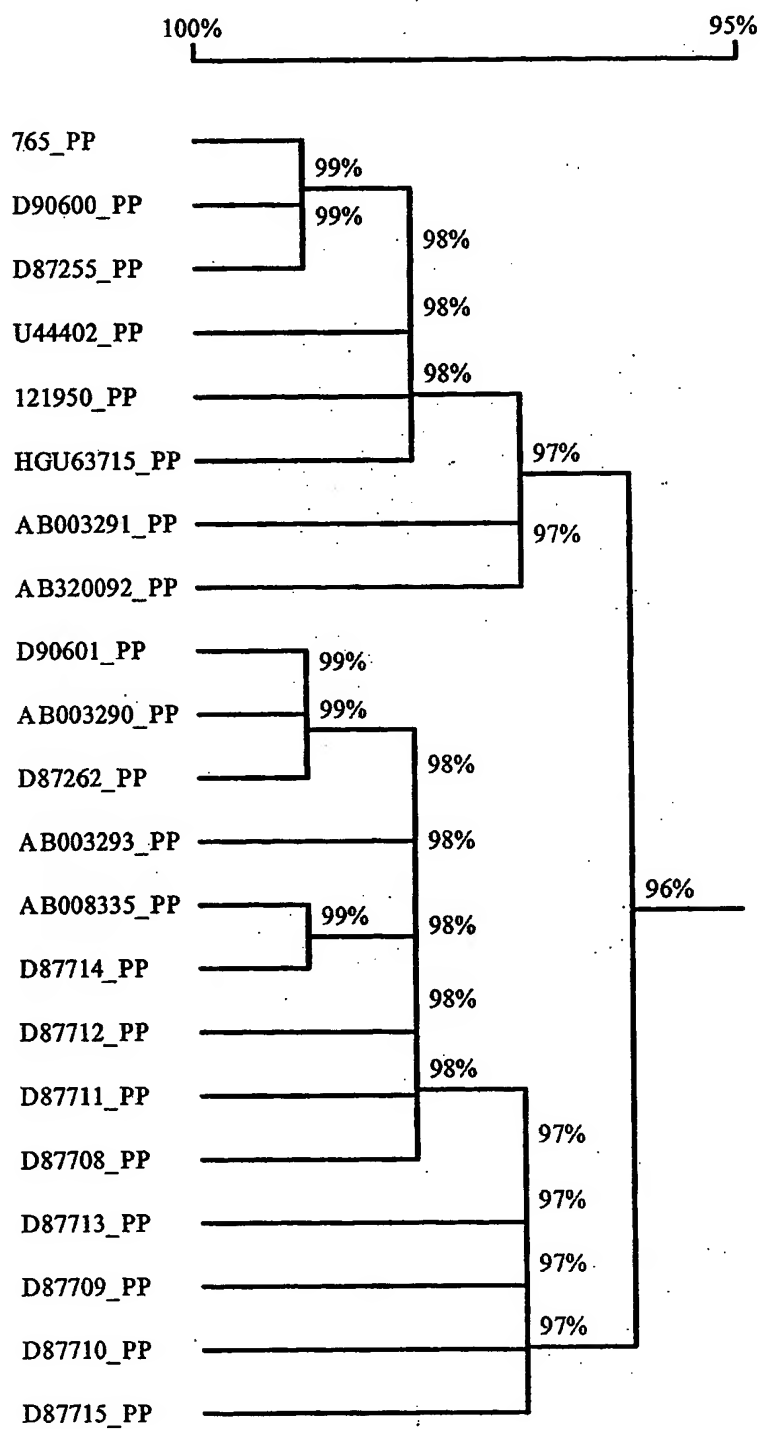
GenBank Accession Number

Except isolate 765

AF121950 = infectious clone sequence



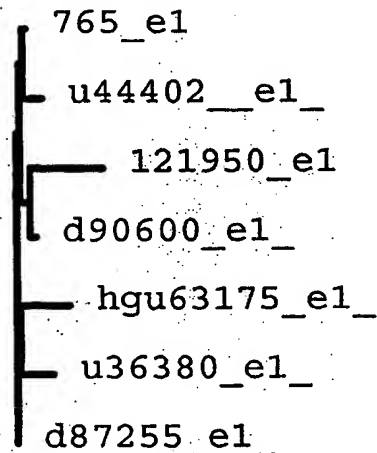
22
Figure 4: GBV-C Polyprotein (pp) Phylogenetic Tree



GBV-C phylogenetic relationships by protein coding region.

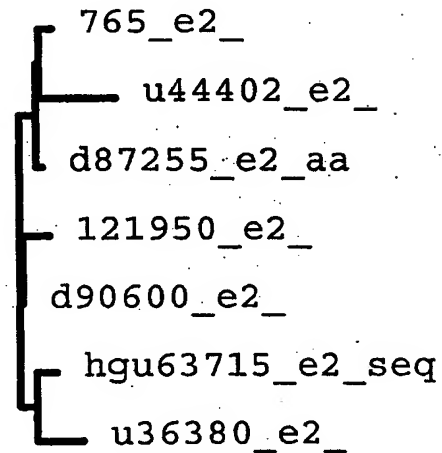
²³
Figure 5A: E1

0.05



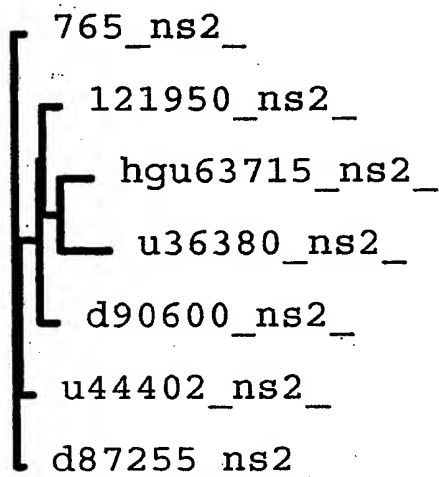
²³
Figure 5B: E2

0.05



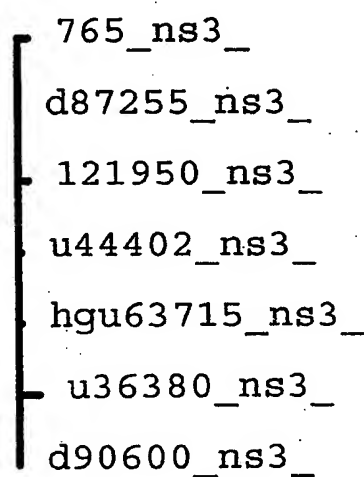
²³
Figure 5C: NS2

0.05



²³
Figure 5D: NS3

0.05



GBV-C phylogenetic relationships by protein coding region.

²³
Figure 5E: NS4

0.05



765_ns4a_
d87255_ns4a_
u44402_ns4a_
121950_ns4a_
hgu63715_ns4a_
u36380_ns4a_
d90600_ns4a_

²³
Figure 5F: NS5A

0.05



765_ns5a
d87255_ns5a_
121950_ns5a_
u44402_ns5a_
hgu63715_ns5a_
d90600_ns5a_

²³
Figure 5G: NS5B

0.05



765_ns5b_
u44402_ns5b_
121950_ns5b_
d90600_ns5b_
d87255_ns5b_
hgu63715_ns5b_

24

Figure 6: GBV-C 765 compared with 21 full-length GBV-C genomes: Unique amino acid mutations

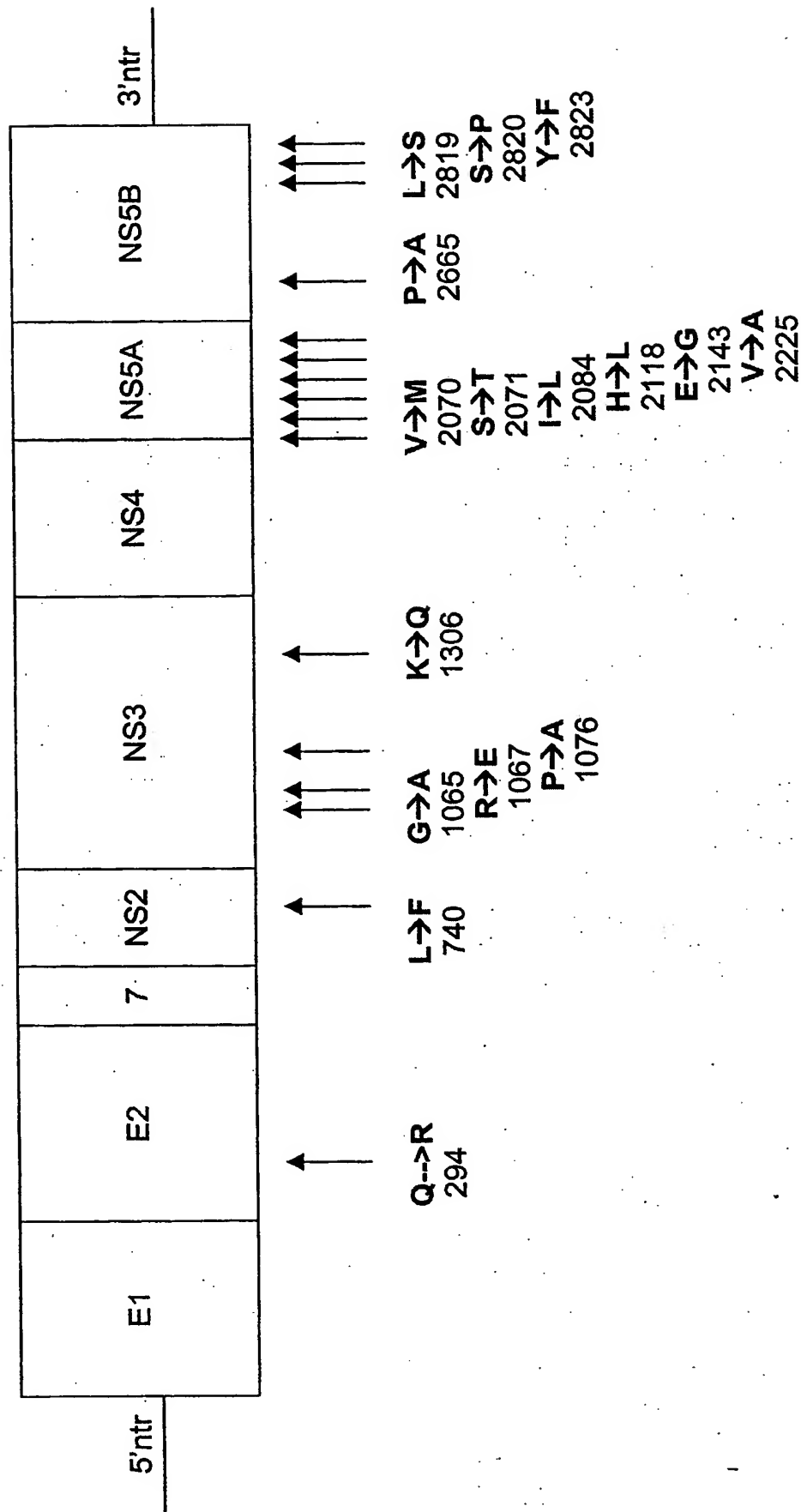


Figure 7: Amino acid substitutions in NS5A region of 765 vs. AF121950

121950	VALVNREPKVDEVQGYVWDLWEWIMRQVRMVMARLRALCPVSLPLWHCGEGWSGE	-----
765		
121950	WLLDGHVESRCLCGCVITGDVLNGQLKDPVYSTKLCRHYWMGTVPVNMLGYGETSPLLA	-----
765		
121950	SDTPKVVPFGTSGWAEVWTPTHVIRRTSAYKLLRQQILSAAVAEPYVVDGIPVSWDADA	-----
765		
121950	RAPAMVYGPQGQSVTIDGERYTLPHQRLRLNVAPSEVSSEVSIDIGTETEDSELTEADLP	-----
765		
121950	AAALQAIENAAARILEPHIDVIMEDCSTPSLCGSSREMPVWGEDIPRTPSPALISVTESSPDE	-----
765		
121950	KTPSVSSSQEDTPSSDSFEVIQSEETAEGEESVFNVALSVLKALFPQSDATRKLTVMKMSCC	-----
765		
121950	VEKSVTRFFSLGLTVADVASLCEMEIQNHTAYCDKVRTPLELQVGCLVGNEILT	-----
765		

Resonance Homologous to the HCV SDR

Figure 1 20

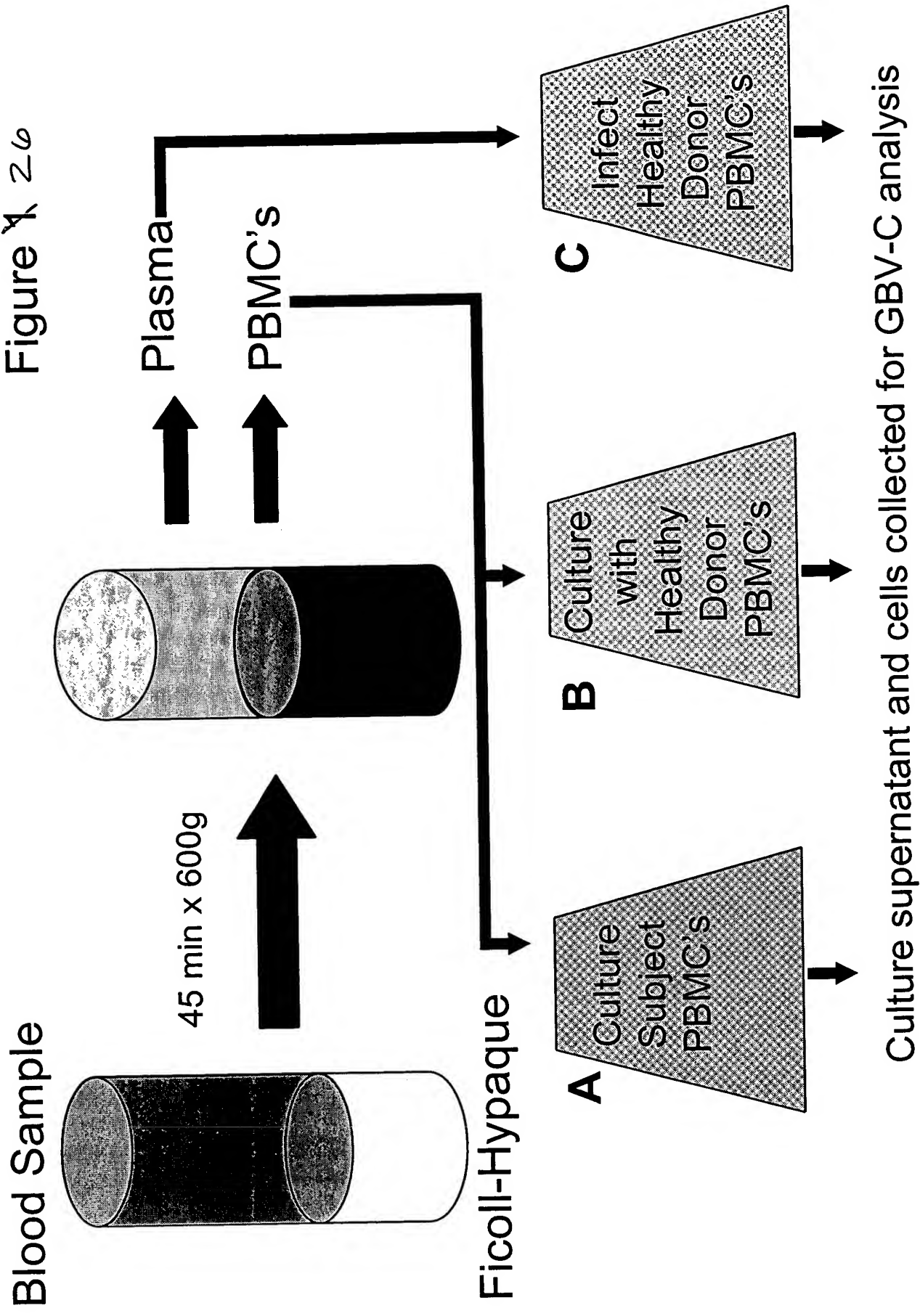


Figure 2A. 27A

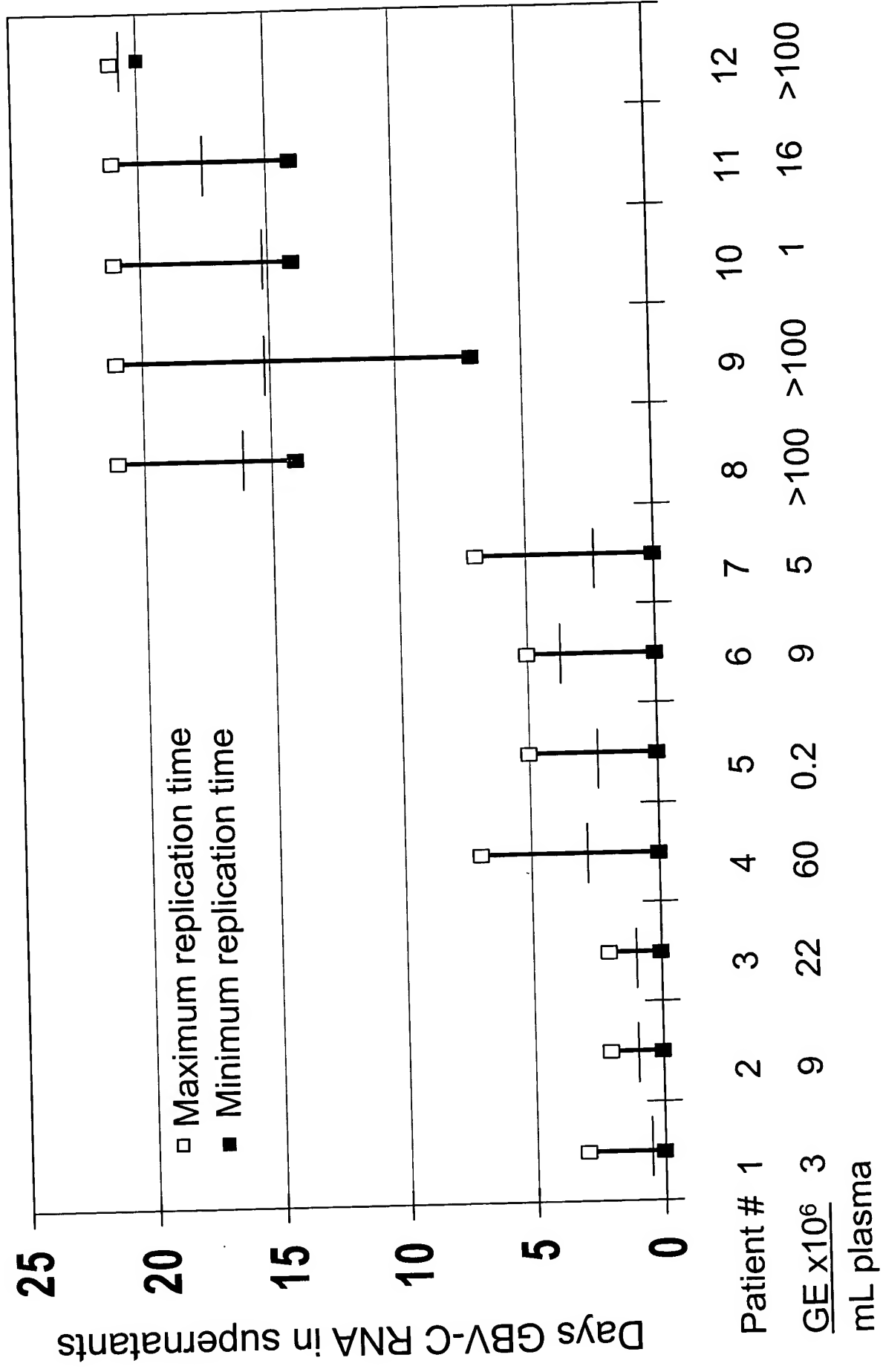


Figure 2B. 27B

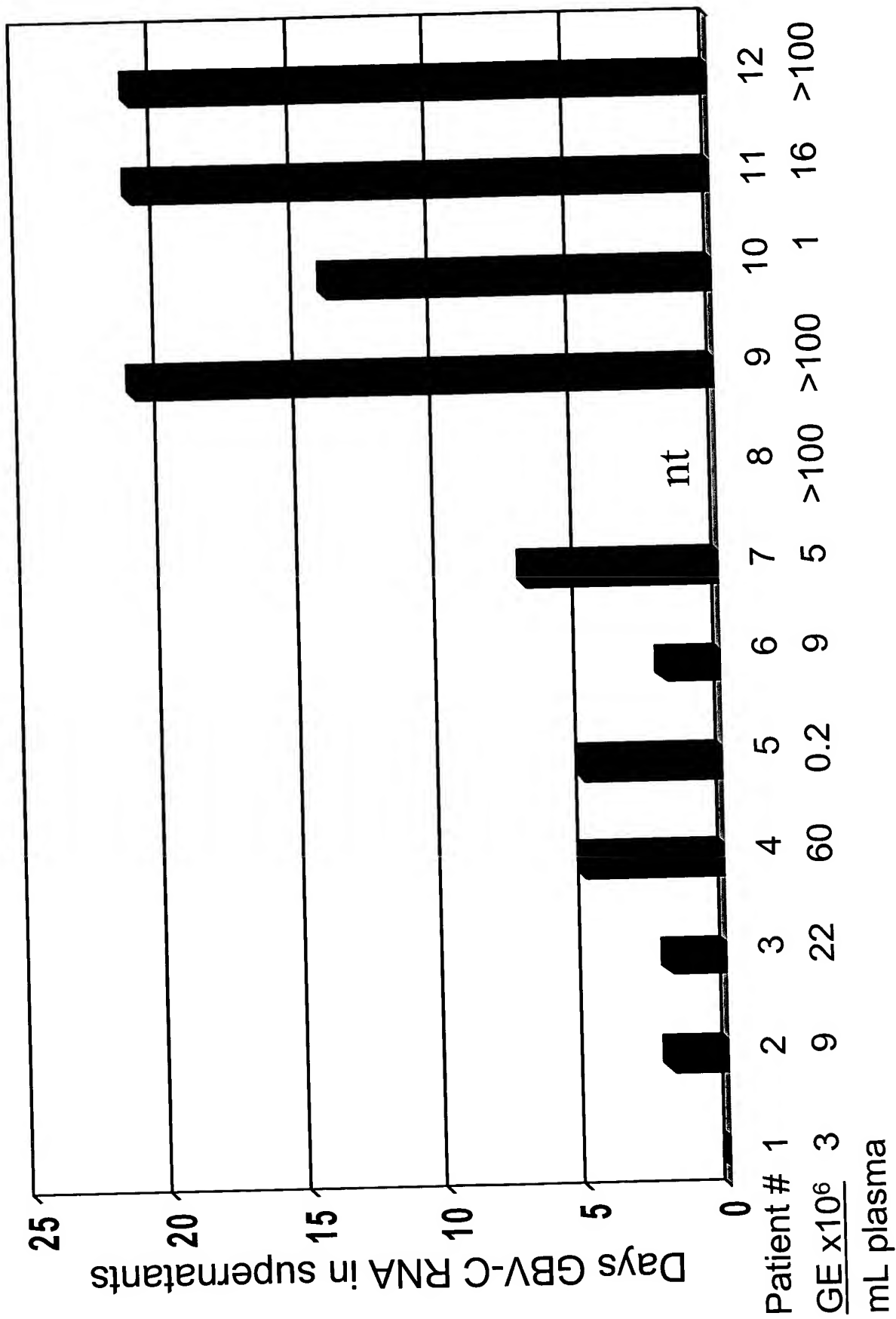


Figure 2C 27C

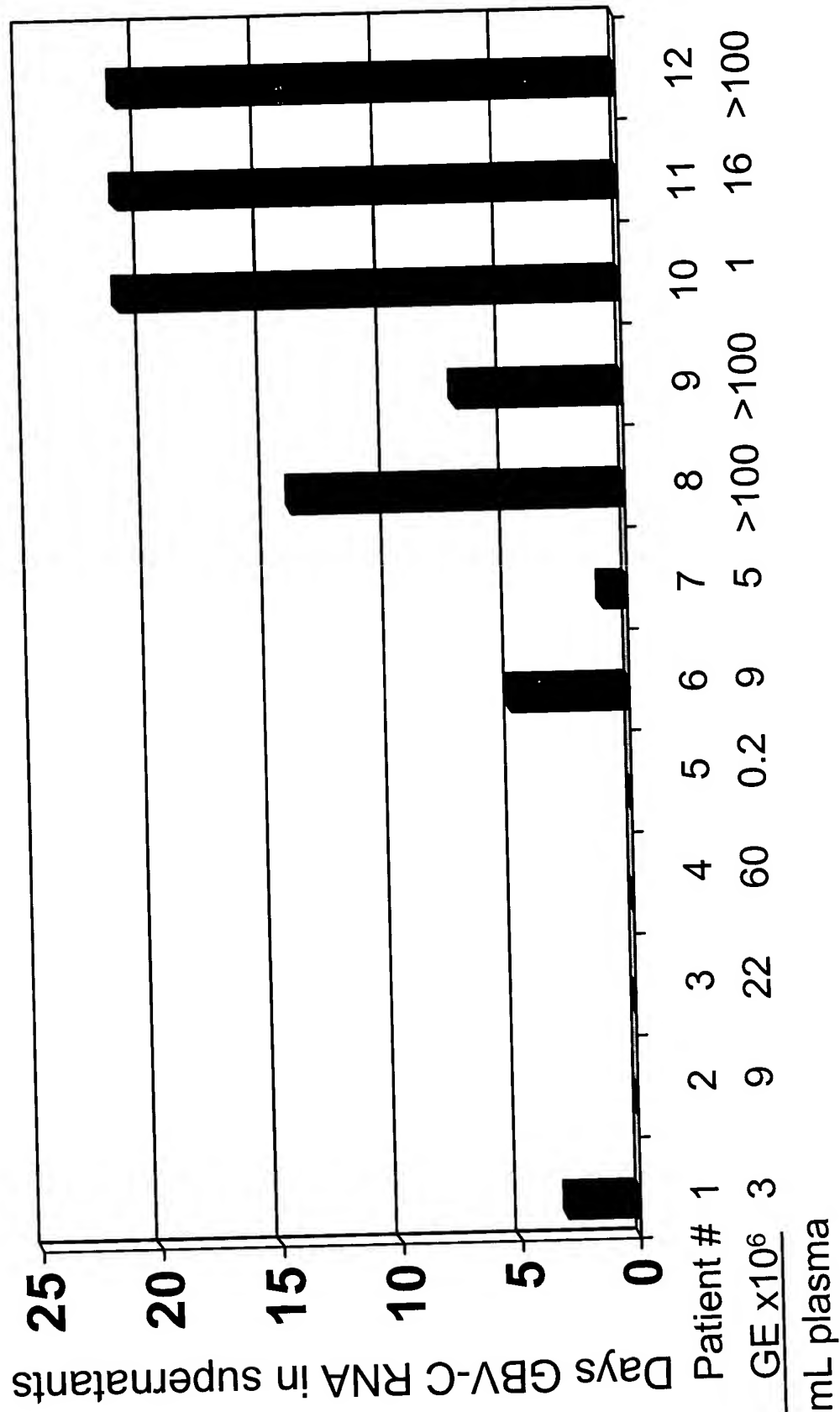


Figure 3 28

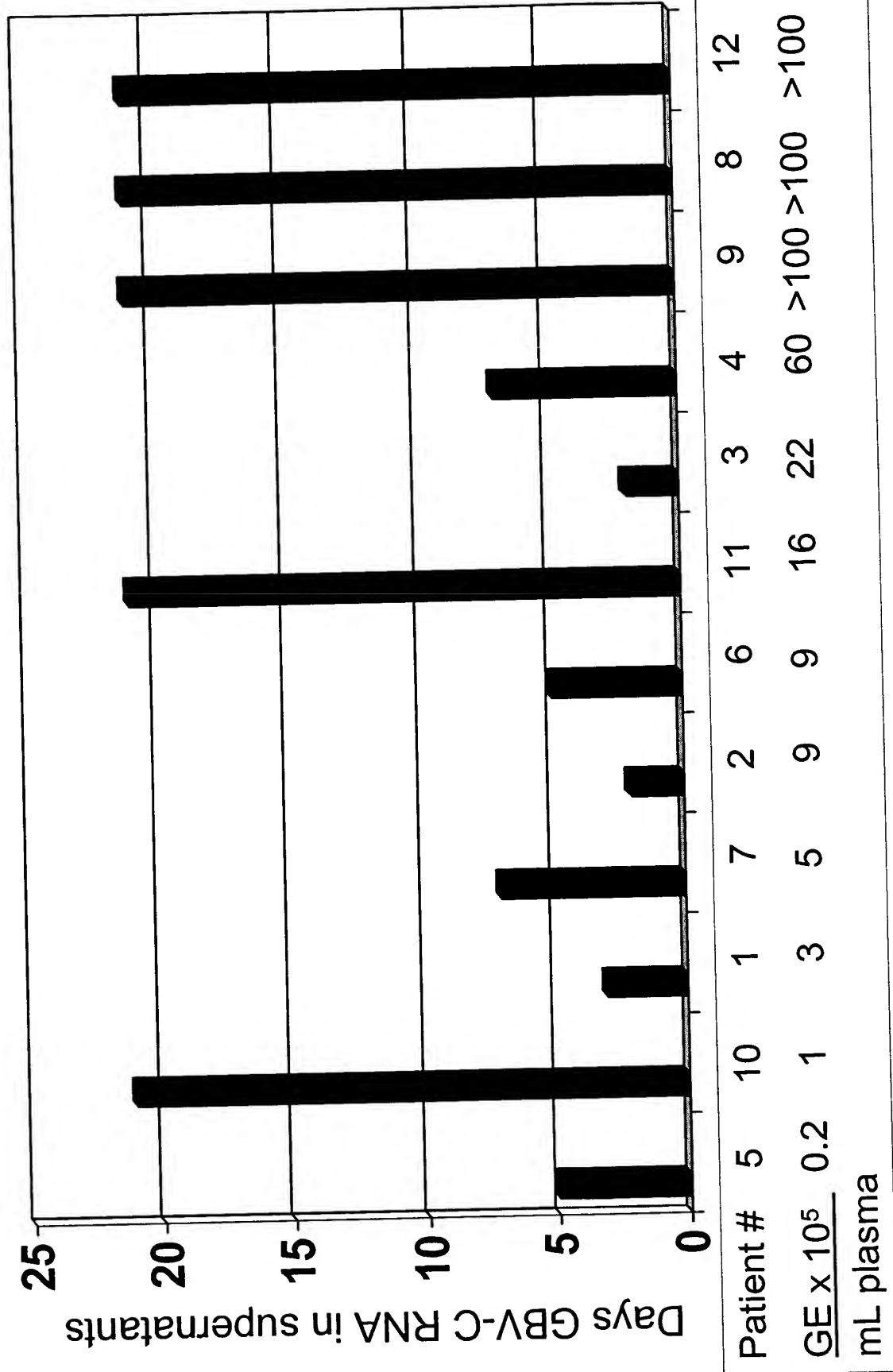


Figure 29

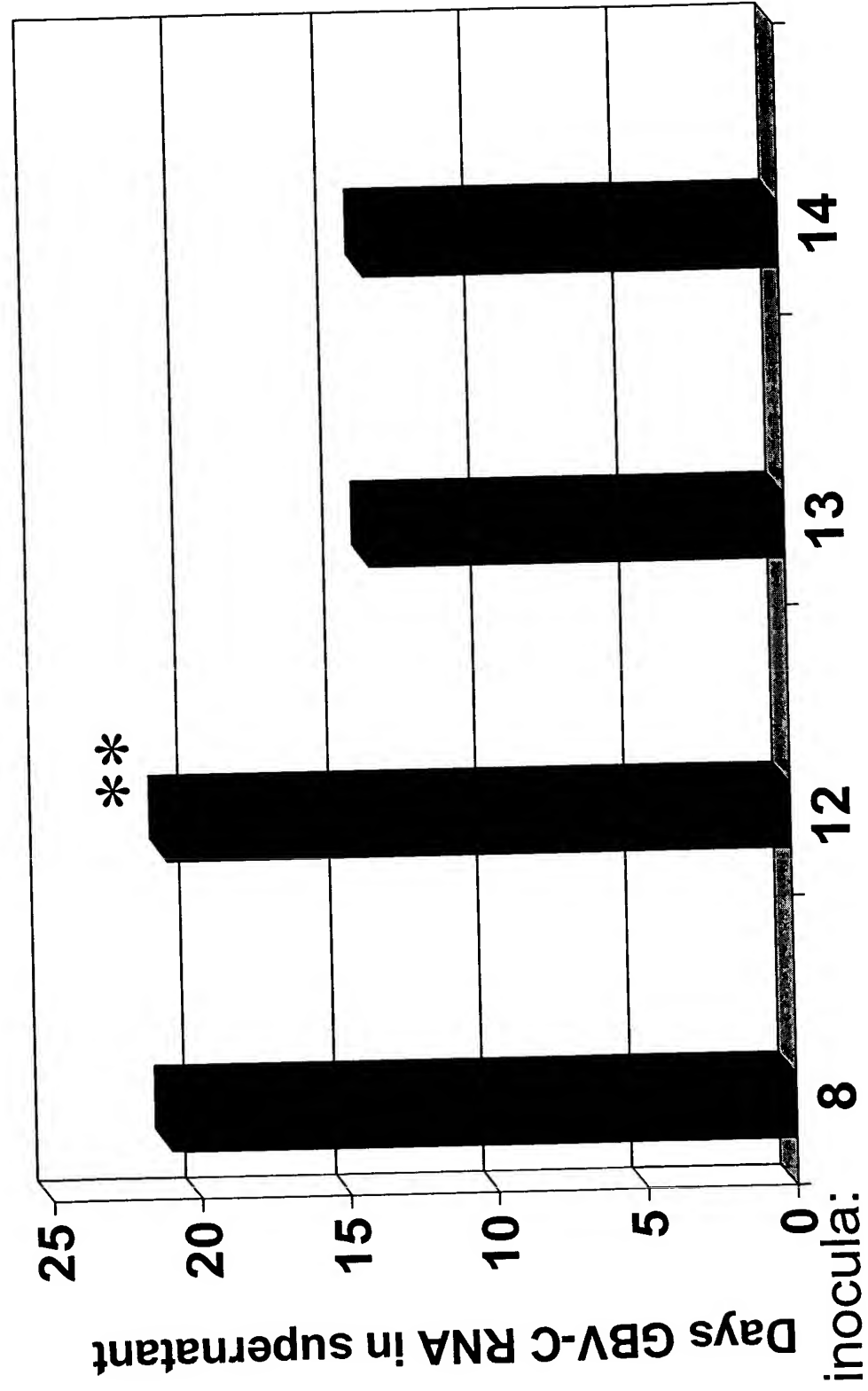
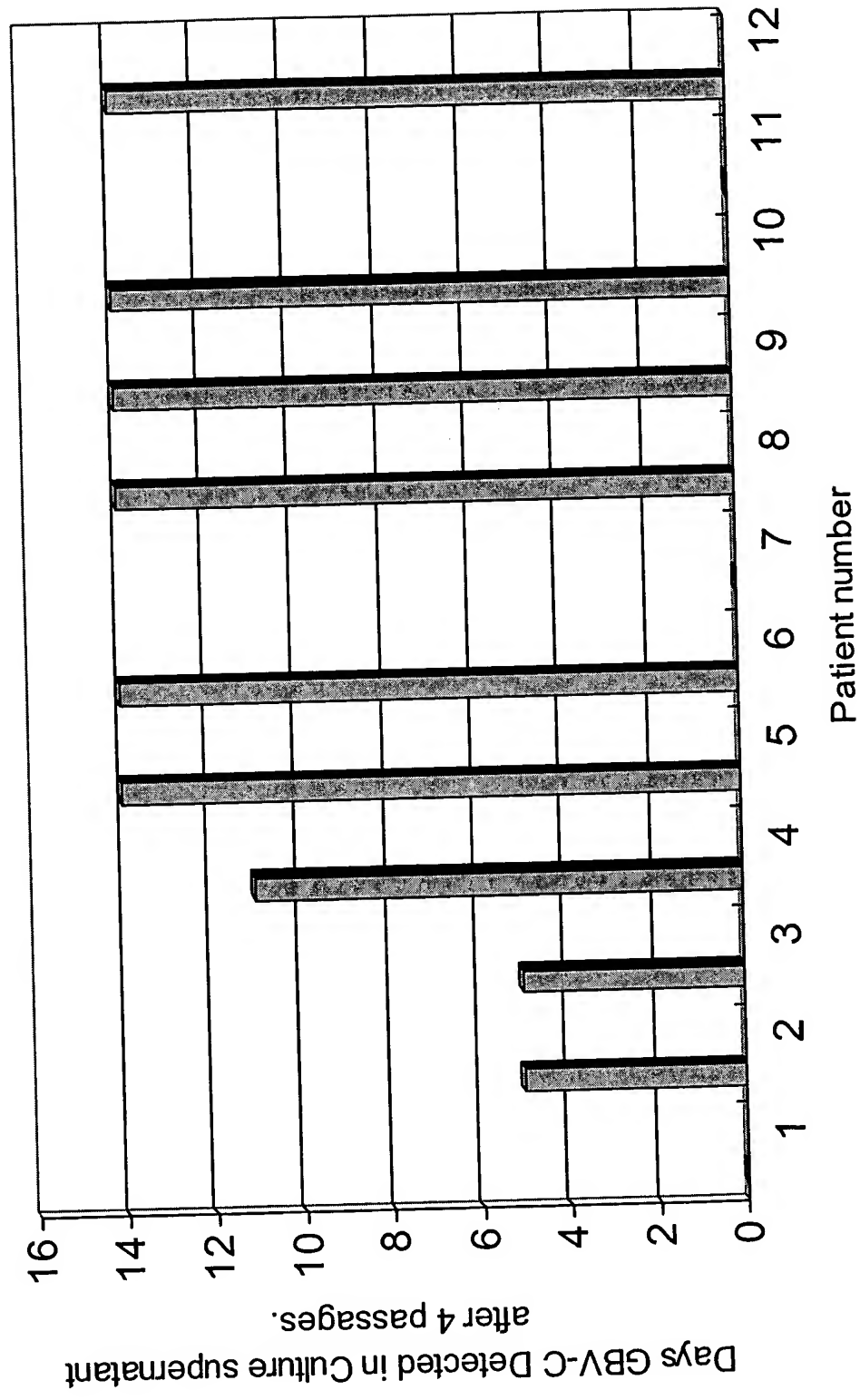


Figure 5.30



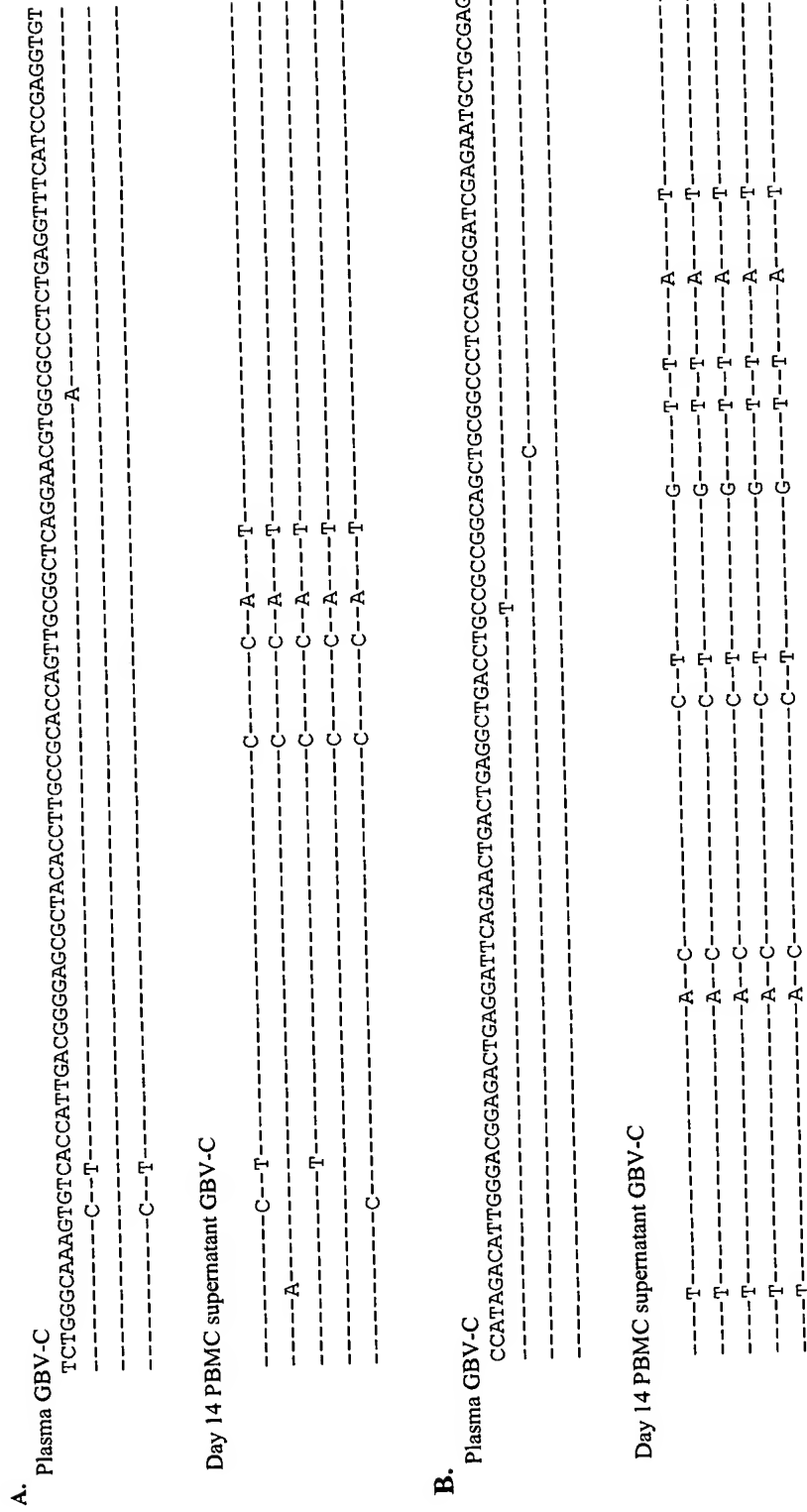


Figure X 32

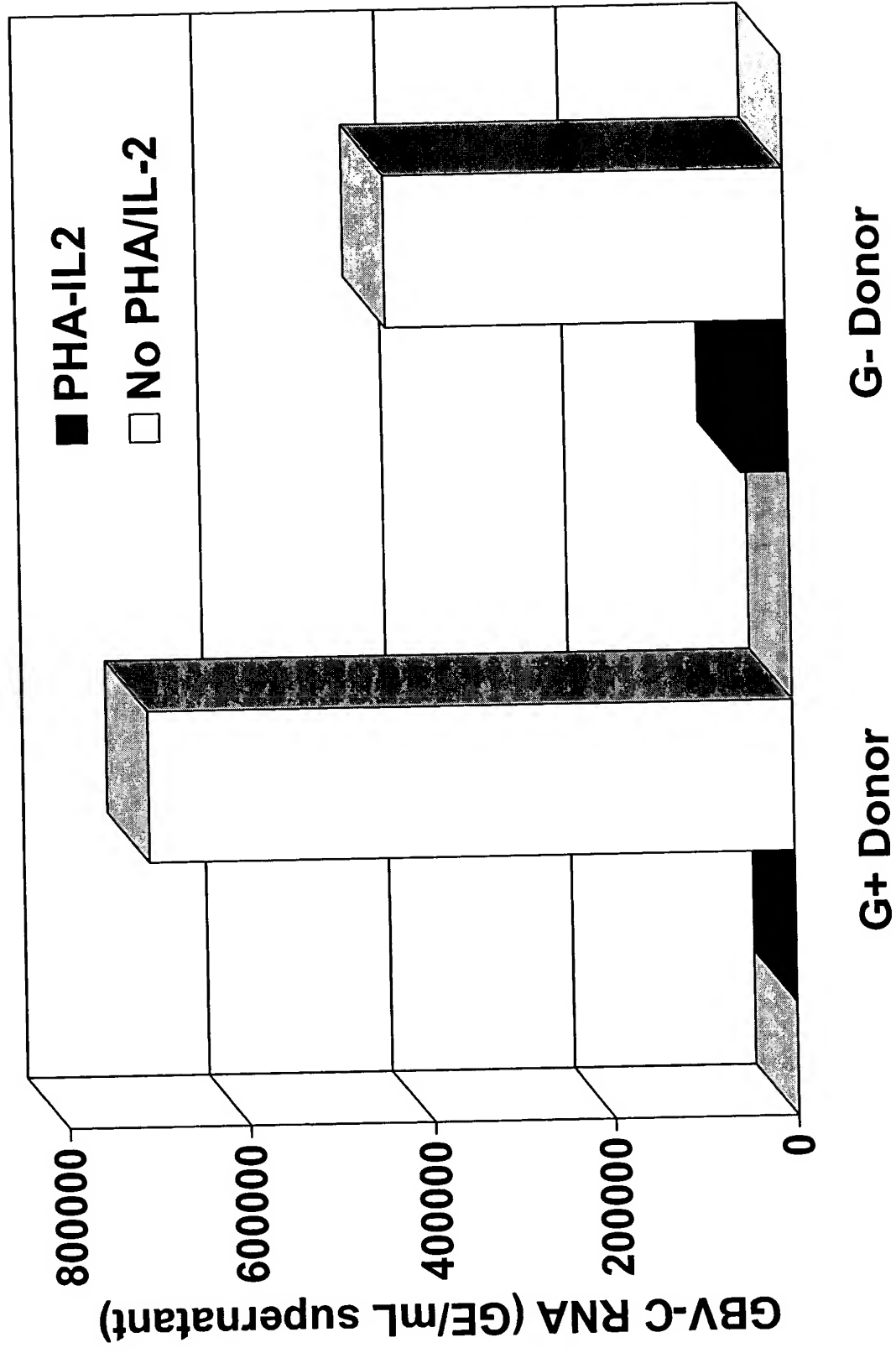


Figure 8 33

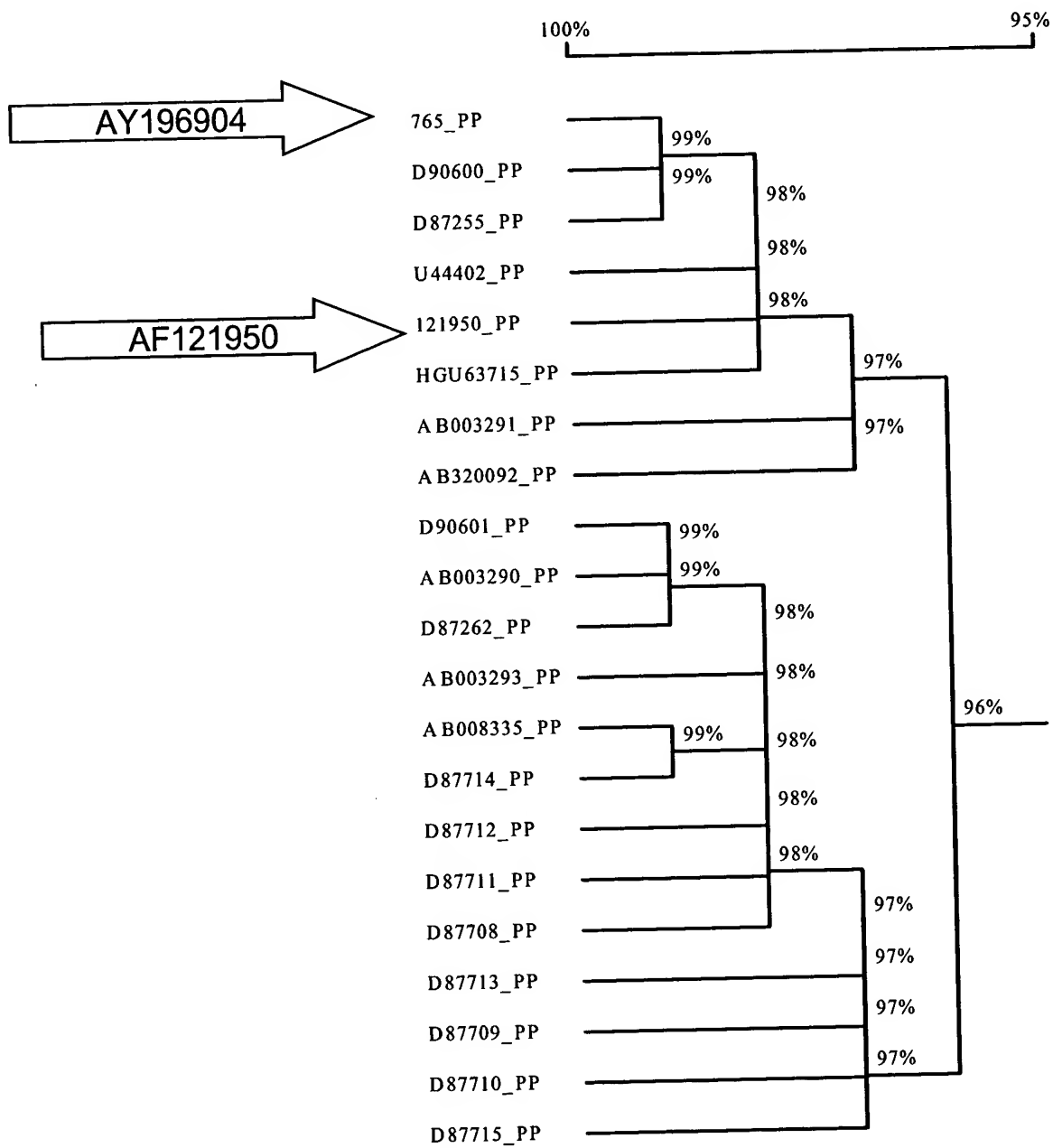


Figure 9A

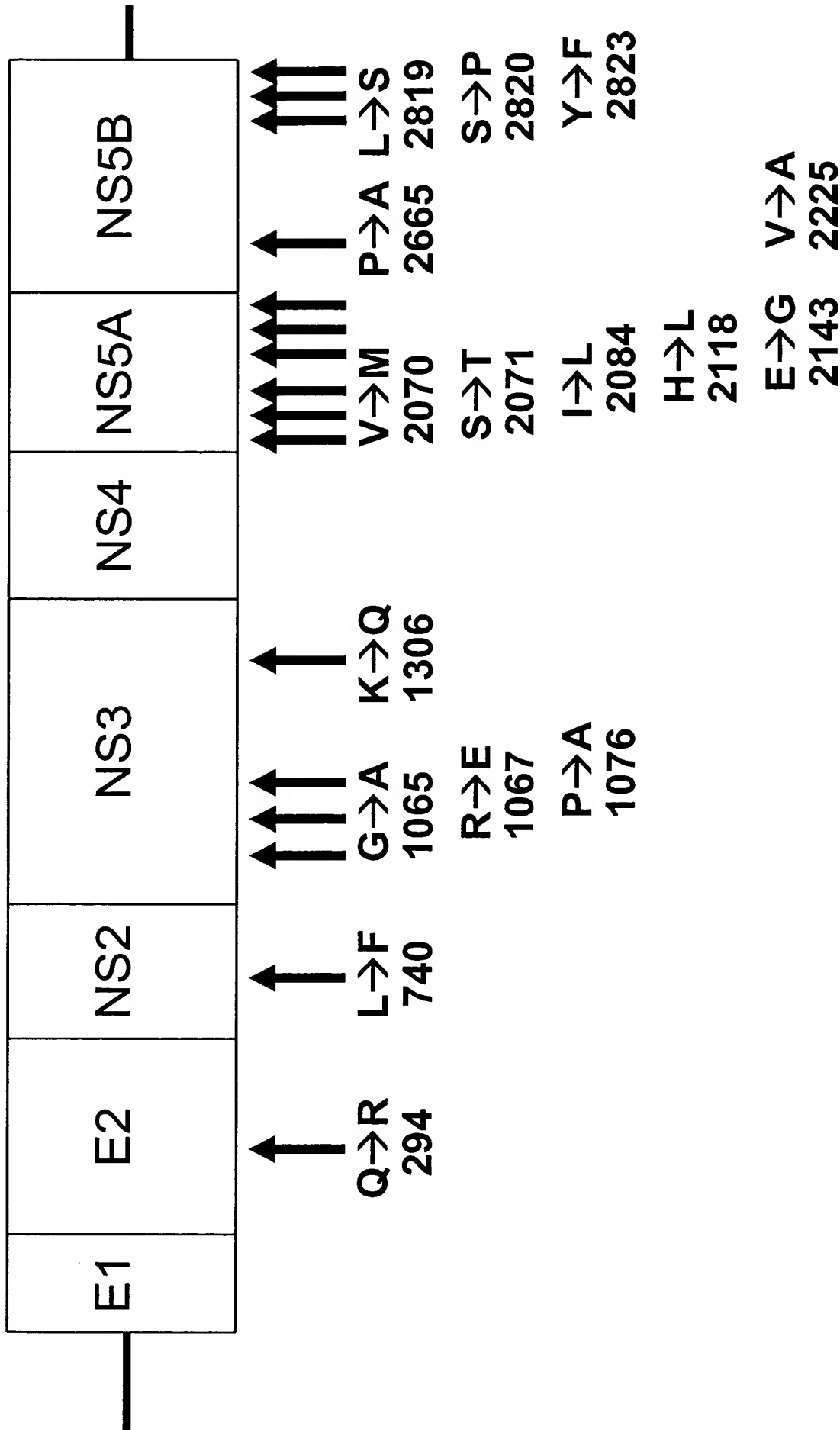


Figure 9B 34 B

AA 2457	AF121950	FQYTPNQRIREMLKL
	AY196904	-----VK-----

AA 2791	AF121950	GIPGAFPLSPPYMGVV
	AY196904	-----G-SP---F----

Figure 9C 34c

121950 VALVNREPKVDEVQGYVWDLWEWIMRQVRMVARLRALCPVVSPLWHCGEGWSGE
196904 -----
121950 WLLDGHVESRCLCGCVITGDLVNGQLKDPVYSTKLCRHYWMGTVPVNMLGYGETSPLLA
196904 -----
121950 SDTPKVVPFGTSGWAEVVVTPTHVVIIRRTSAYKLLRQQLSAAVAEPYYVDGIPVSWDADA
196904 -----
121950 RAPAMVYGPQSVTIDGERYTLPHQLRLRNVAPEVSSEVSIDIGTETEDSELTEADLPPA
196904 -----
121950 AAALQAIENAARILEPHIDVIMEDCSTPSLCGSSREMPVWGEDIPTPTSPALISVTESSPDE
196904 -----
121950 KTPSVSSSQEDTPSSDSFEVIQSESETAEGEESVFNVALSVLKALFPQSDATRKLTVKMSCC
196904 -----
121950 VEKSVTRFFSLGLTVADVASLCEMEIQNHHTAYCDKVRTPLELQVGCIVGNELT
196904 A-----

|Region homologous to the HCV ISDR|

MT-L

G

L

S